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SEQUENCE LISTING

RECEIVED  
TECH CENTER 1600/2900  
03 JAN 30 AM 10:48

(1) GENERAL INFORMATION:

- (i) APPLICANT: Recombinant Biocatalysis, Inc.
- (ii) TITLE OF INVENTION: THERMOSTABLE PHOSPHATASES
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Fish & Richardson P.C.
  - (B) STREET: 4225 Executive Square, Suite 1400
  - (C) CITY: La Jolla
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: Windows 95
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US97/10784
  - (B) FILING DATE: 19-JUN-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/666,857
  - (B) FILING DATE: 19-JUN-1996
  - (A) APPLICATION NUMBER: 60/033,752
  - (B) FILING DATE: 19-JUN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Haile, Ph.D., Lisa A.
  - (B) REGISTRATION NUMBER: 38,347
  - (C) REFERENCE/DOCKET NUMBER: 09010/015WO1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 619/678-5070
  - (B) TELEFAX: 619/678-5099
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGGGGGCA GGTCCGAAAA GG

52

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGAGGATCC TCACCGCCCC CTGCGGGTGC G

31

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGTTGGAT ATACTGCTTG TT

52

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCGACGATCC TTATTTTSTA ACCAAATGTT CC

32

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGATGATG GAATTCATC GC

52

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAGGATCC CTACAGTTCT AAAAGTCTTT TA

32

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGAGAACC CTGACAATAA AC

52

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGAGGATCC TTACACCCAC AGAACCTTA C

31

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAAAGGA AAGTCTCTTG TT

52

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGAGGATCC TCAAGCTTCC TGGAGAATCA A

31

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGCCAAGA AATATCGCCG CT 52

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGAGGATCC TTAAGGCTTC TCGAGGTGGG GGTT 34

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGTATAAA TGGATTATTG AGGG 54

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCGAGGACTA AACATAGTCT AAGTAATTAG C 31

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAGAATC CTCCTCACCA AC 52

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGAGGATCC TCACAGGCTC AGAAGCCTTT G

31

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGGAAAAC TTAAAAAAGT ACCT

54

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGAGGATCC TCACCGCCCC CTGCGGGTGC G

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG AGG GGG AGC GGA GTG CGG ATA CTT CTC ACC AAC GAT GAC GGC ATC  
Met Arg Gly Ser Gly Val Arg Ile Leu Leu Thr Asn Asp Asp Gly Ile  
1 5 10 15

48

TTT GCC GAG GGT CTG GGG GCT CTG CGC AAG ATG CTG GAG CCC GTG GCT  
Phe Ala Glu Gly Leu Gly Ala Leu Arg Lys Met Leu Glu Pro Val Ala  
20 25 30

96

ACC CTT TAC GTG GTG GCT CCG GAC CGA GAG CGT AGC GCG GCC AGC CAT  
Thr Leu Tyr Val Val Ala Pro Asp Arg Glu Arg Ser Ala Ala Ser His

144

35					40					45						
GCT	ATC	ACC	GTT	CAC	CGC	CCC	CTG	CGG	GTG	CGG	GAG	GCG	GGT	TTT	CGC	192
Ala	Ile	Thr	Val	His	Arg	Pro	Leu	Arg	Val	Arg	Glu	Ala	Gly	Phe	Arg	
	50					55					60					
AGC	CCC	AGG	CTT	AAA	GGC	TGG	GTA	GTG	GAC	GGT	ACC	CCG	GCC	GAC	TGC	240
Ser	Pro	Arg	Leu	Lys	Gly	Trp	Val	Val	Asp	Gly	Thr	Pro	Ala	Asp	Cys	
	65					70					75				80	
GTC	AAG	CTG	GGC	CTG	GAG	GTA	CTT	TTG	CCC	GAA	CGT	CCA	GAT	TTC	CTG	288
Val	Lys	Leu	Gly	Leu	Glu	Val	Leu	Leu	Pro	Glu	Arg	Pro	Asp	Phe	Leu	
				85					90					95		
GTT	TCG	GGC	ATA	AAC	TAC	GGG	CCC	AAC	CTG	GGT	ACC	GAC	GTA	CTT	TAC	336
Val	Ser	Gly	Ile	Asn	Tyr	Gly	Pro	Asn	Leu	Gly	Thr	Asp	Val	Leu	Tyr	
			100					105					110			
TCC	GGC	ACC	GTC	TCG	GCG	GCC	ATA	GAA	GGG	GTA	ATT	AAC	GGC	ATT	CCC	384
Ser	Gly	Thr	Val	Ser	Ala	Ala	Ile	Glu	Gly	Val	Ile	Asn	Gly	Ile	Pro	
			115				120					125				
TCG	GTG	GCC	GTA	TCT	TTG	GCC	ACG	CGG	CGG	GAG	CCG	GAC	TAT	ACC	TGG	432
Ser	Val	Ala	Val	Ser	Leu	Ala	Thr	Arg	Arg	Glu	Pro	Asp	Tyr	Thr	Trp	
	130					135					140					
GCG	GCC	CGG	TTC	GTC	CTG	GTC	CTG	CTG	GAG	GAA	CTG	CGA	AAA	CAC	CAA	480
Ala	Ala	Arg	Phe	Val	Leu	Val	Leu	Leu	Glu	Glu	Leu	Arg	Lys	His	Gln	
	145					150					155				160	
CTG	CCC	CCA	GGA	ACC	CTG	CTC	AAC	GTC	AAC	GTG	CCC	GAC	GGG	GTG	CCC	528
Leu	Pro	Pro	Gly	Thr	Leu	Leu	Asn	Val	Asn	Val	Pro	Asp	Gly	Val	Pro	
				165					170					175		
CGC	GGG	GTC	AAG	GTG	ACC	AAA	CTG	GGA	AGC	GTA	CGC	TAC	GTC	AAC	GTG	576
Arg	Gly	Val	Lys	Val	Thr	Lys	Leu	Gly	Ser	Val	Arg	Tyr	Val	Asn	Val	
			180					185					190			
GTA	GAC	TGC	CGC	ACC	GAC	CCT	CGG	GGG	AAG	GCT	TAC	TAC	TGG	ATG	GCG	624
Val	Asp	Cys	Arg	Thr	Asp	Pro	Arg	Gly	Lys	Ala	Tyr	Tyr	Trp	Met	Ala	
		195					200					205				
GGA	GAA	CCA	TTG	GAG	CTG	GAC	GGC	AAC	GAC	TCC	GAA	ACC	GAC	GTC	TGG	672
Gly	Glu	Pro	Leu	Glu	Leu	Asp	Gly	Asn	Asp	Ser	Glu	Thr	Asp	Val	Trp	
	210					215					220					
GCG	GTG	CGA	GAA	GGC	TAT	ATT	TCC	GTA	ACA	CCG	GTC	CAG	ATC	GAC	CTT	720
Ala	Val	Arg	Glu	Gly	Tyr	Ile	Ser	Val	Thr	Pro	Val	Gln	Ile	Asp	Leu	
	225					230					235				240	
ACT	AAC	TAC	GGC	TTC	CTG	GAA	GAA	CTC	AAA	AAA	TGG	CGT	TTC	AAG	GAT	768
Thr	Asn	Tyr	Gly	Phe	Leu	Glu	Glu	Leu	Lys	Lys	Trp	Arg	Phe	Lys	Asp	
				245					250					255		
ATC	TTT	TCT	TCT	TAA												783
Ile	Phe	Ser	Ser													
			260													

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG TTG GAT ATA CTG CTT GTT AAT GAT GAT GGC ATT TAT TCA AAT GGA	48
Met Leu Asp Ile Leu Leu Val Asn Asp Asp Gly Ile Tyr Ser Asn Gly	
1 5 10 15	
TTA ATA GCT TTG AAG GAT GCA TTA TTG GAA AAA TTT AAT GCG AGG ATT	96
Leu Ile Ala Leu Lys Asp Ala Leu Leu Glu Lys Phe Asn Ala Arg Ile	
20 25 30	
ACT ATT GTA GCC CCA ACA AAT CAG CAG AGT GGT ATT GGT AGG GCA ATA	144
Thr Ile Val Ala Pro Thr Asn Gln Gln Ser Gly Ile Gly Arg Ala Ile	
35 40 45	
AGT TTA TTC GAG CCG TTA AGG ATA ACT AAA ACC AAA TTA GCA GAT GGT	192
Ser Leu Phe Glu Pro Leu Arg Ile Thr Lys Thr Lys Leu Ala Asp Gly	
50 55 60	
TCT TGG GGA TAT GCA GTT TCA GGA ACC CCA ACA GAT TGC GTT ATA TTG	240
Ser Trp Gly Tyr Ala Val Ser Gly Thr Pro Thr Asp Cys Val Ile Leu	
65 70 75 80	
GGC ATT TAT GAG ATA TTA AAG AAG GTA CCT GAT GTA GTT ATA TCA GGA	288
Gly Ile Tyr Glu Ile Leu Lys Lys Val Pro Asp Val Val Ile Ser Gly	
85 90 95	
ATA AAC ATT GGA GAA AAC CTT GGG ACT GAA ATA ACA ACT TCT GGA ACG	336
Ile Asn Ile Gly Glu Asn Leu Gly Thr Glu Ile Thr Thr Ser Gly Thr	
100 105 110	
TTG GGG GCT GCG TTT GAA GGG GCC CAT CAT GGG GCT AAG GCA TTA GCA	384
Leu Gly Ala Ala Phe Glu Gly Ala His His Gly Ala Lys Ala Leu Ala	
115 120 125	
TCA TCA CTC CAA GTT ACC TCT GAC CAT CTA AAG TTT AAA GAG GGG GAG	432
Ser Ser Leu Gln Val Thr Ser Asp His Leu Lys Phe Lys Glu Gly Glu	
130 135 140	
ACC CCA ATA GAC TTC ACA GTC CCA GCA AGA ATT ACT GCA AAT GTT GTT	480
Thr Pro Ile Asp Phe Thr Val Pro Ala Arg Ile Thr Ala Asn Val Val	
145 150 155 160	
GAG AAG ATG TTG GAT TAT GAT TTC CCA TGT GAT GTC GTC AAC TTA AAC	528
Glu Lys Met Leu Asp Tyr Asp Phe Pro Cys Asp Val Val Asn Leu Asn	
165 170 175	
ATT CCA GAA GGA GCA ACA GAA AAG ACA CCG ATT GAA ATC ACA AGG TTG	576
Ile Pro Glu Gly Ala Thr Glu Lys Thr Pro Ile Glu Ile Thr Arg Leu	
180 185 190	
GCA AGG AAA ATG TAT ACA ACA CAC GTT GAG GAA AGA ATA GAT CCA AGA	624
Ala Arg Lys Met Tyr Thr Thr His Val Glu Glu Arg Ile Asp Pro Arg	
195 200 205	
GGG AGG AGT TAT TAT TGG ATT GAT GGG TAT CCT ATT TTA GAG GAA GAG	672
Gly Arg Ser Tyr Tyr Trp Ile Asp Gly Tyr Pro Ile Leu Glu Glu Glu	
210 215 220	

GAA GAC ACT GAT GTC TAT GTT GTT AGA AGA AAG GGA CAT ATT TCT CTA	720
Glu Asp Thr Asp Val Tyr Val Val Arg Arg Lys Gly His Ile Ser Leu	
225 230 235 240	
ACC CCA TTA ACA TTA GAC ACA ACA ATT AAA AAT TTA GAG GAA TTT AAG	768
Thr Pro Leu Thr Leu Asp Thr Thr Ile Lys Asn Leu Glu Glu Phe Lys	
245 250 255	
AAA AAA TAT GAG AGA ATA TTA AAT GAA TGA	798
Lys Lys Tyr Glu Arg Ile Leu Asn Glu	
260 265	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATG ATG ATG GAA TTC ACT CGC GAG GGA ATA AAA GCT GCT GTA GAG GCA	48
Met Met Met Glu Phe Thr Arg Glu Gly Ile Lys Ala Ala Val Glu Ala	
1 5 10 15	
CTT CAA GGG TTA GGA GAG ATC TAC GTA GTT GCC CCA ATG TTT CAA AGG	96
Leu Gln Gly Leu Gly Glu Ile Tyr Val Val Ala Pro Met Phe Gln Arg	
20 25 30	
AGC GCA AGT GGA AGG GCA ATG ACC ATC CAC AGA CCT CTA AGG GCT AAA	144
Ser Ala Ser Gly Arg Ala Met Thr Ile His Arg Pro Leu Arg Ala Lys	
35 40 45	
AGA ATA AGT ATG AAC GGT GCA AAA GCA GCC TAT GCT TTG GAT GGA ATG	192
Arg Ile Ser Met Asn Gly Ala Lys Ala Ala Tyr Ala Leu Asp Gly Met	
50 55 60	
CCC GTT GAT TGC GTT ATC TTT GCC ATG GCC AGA TTT GGA GAT TTC GAC	240
Pro Val Asp Cys Val Ile Phe Ala Met Ala Arg Phe Gly Asp Phe Asp	
65 70 75 80	
CTT GCA ATA AGT GGT GTA AAC TTG GGA GAA AAC ATG AGC ACC GAG ATA	288
Leu Ala Ile Ser Gly Val Asn Leu Gly Glu Asn Met Ser Thr Glu Ile	
85 90 95	
ACG GTT TCC GGG ACT GCA AGC GCT GCA ATA GAG GCT GCA ACC CAA GAG	336
Thr Val Ser Gly Thr Ala Ser Ala Ala Ile Glu Ala Ala Thr Gln Glu	
100 105 110	
ATC CCA AGC ATT CCC ATA AGC CTG GAA GTT AAT AGA GAA AAA CAC AAA	384
Ile Pro Ser Ile Pro Ile Ser Leu Glu Val Asn Arg Glu Lys His Lys	
115 120 125	
TTT GGT GAG GGC GAA GAG ATT GAC TTC TCA GCT GCC AAG TAT TTC CTA	432
Phe Gly Glu Gly Glu Glu Ile Asp Phe Ser Ala Lys Tyr Phe Leu	
130 135 140	
AGA AAA ATC GCA ACG GCG GTT TTA AAG AGA GGC CTC CCC AAA GGA GTC	480

Arg	Lys	Ile	Ala	Thr	Ala	Val	Leu	Lys	Arg	Gly	Leu	Pro	Lys	Gly	Val	
145					150					155					160	
GAT	ATG	CTG	AAC	GTC	AAC	GTC	CCT	TAT	GAT	GCA	AAT	GAA	AGG	ACA	GAG	528
Asp	Met	Leu	Asn	Val	Asn	Val	Pro	Tyr	Asp	Ala	Asn	Glu	Arg	Thr	Glu	
				165					170					175		
ATA	GCT	TTT	ACT	CGC	CTG	GCA	AGA	AGG	ATG	TAT	AGG	CCT	TCT	ATT	GAA	576
Ile	Ala	Phe	Thr	Arg	Leu	Ala	Arg	Arg	Met	Tyr	Arg	Pro	Ser	Ile	Glu	
			180					185					190			
GAG	CGC	ATA	GAC	CCA	AAG	GGG	AAT	CCC	TAC	TAC	TGG	ATA	GTT	GGA	ACT	624
Glu	Arg	Ile	Asp	Pro	Lys	Gly	Asn	Pro	Tyr	Tyr	Trp	Ile	Val	Gly	Thr	
		195					200					205				
CAG	TGC	CCT	AAG	GAG	GCA	TTA	GAG	CCG	GGA	ACG	GAT	ATG	TAT	GTA	GTT	672
Gln	Cys	Pro	Lys	Glu	Ala	Leu	Glu	Pro	Gly	Thr	Asp	Met	Tyr	Val	Val	
	210					215					220					
AAA	GTT	GAG	AGA	AAA	GTT	AGC	GTG	ACT	CCA	ATA	AAC	ATT	GAT	ATG	ACA	720
Lys	Val	Glu	Arg	Lys	Val	Ser	Val	Thr	Pro	Ile	Asn	Ile	Asp	Met	Thr	
225					230					235					240	
GCA	AGA	GTG	AAT	TTA	GAC	GAG	ATT	AAA	AGA	CTT	TTA	GAA	CTG			762
Ala	Arg	Val	Asn	Leu	Asp	Glu	Ile	Lys	Arg	Leu	Leu	Glu	Leu			
				245					250							
TAG																765

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG	AGA	ACC	CTG	ACA	ATA	AAC	ACT	GAC	GCG	GAG	GGG	TTC	GTT	TTG	AGG	48
Met	Arg	Thr	Leu	Thr	Ile	Asn	Thr	Asp	Ala	Glu	Gly	Phe	Val	Leu	Arg	
1				5					10					15		
ATT	CTC	CTG	ACG	AAC	GAC	GAT	GGA	ATC	TAC	TCC	AAC	GGA	CTG	CGC	GCC	96
Ile	Leu	Leu	Thr	Asn	Asp	Asp	Gly	Ile	Tyr	Ser	Asn	Gly	Leu	Arg	Ala	
			20				25						30			
GCT	GTG	AAA	GCC	CTG	AGT	GAG	CTC	GGC	GAA	GTT	TAC	GTC	GTT	GCC	CCC	144
Ala	Val	Lys	Ala	Leu	Ser	Glu	Leu	Gly	Glu	Val	Tyr	Val	Val	Ala	Pro	
		35					40					45				
CTC	TTC	CAG	AGG	AGC	GCG	AGC	GGC	AGG	GCC	ATG	ACG	CTC	CAC	AGG	CCG	192
Leu	Phe	Gln	Arg	Ser	Ala	Ser	Gly	Arg	Ala	Met	Thr	Leu	His	Arg	Pro	
	50					55					60					
ATA	AGG	GCC	AAG	CGC	GTT	GAC	GTT	CCC	GGC	GCA	AAG	ATA	GCC	TAC	GGA	240
Ile	Arg	Ala	Lys	Arg	Val	Asp	Val	Pro	Gly	Ala	Lys	Ile	Ala	Tyr	Gly	
65					70				75						80	

ATA GAT GGA ACT CCT ACT GAC TGC GTG ATT TTC GCC ATA GCC CGC TTC	288
Ile Asp Gly Thr Pro Thr Asp Cys Val Ile Phe Ala Ile Ala Arg Phe	
85 90 95	
GGG AGC TTT GGT TTA GCC GTG AGC GGG ATT AAC CTC GGC GAG AAC CTG	336
Gly Ser Phe Gly Leu Ala Val Ser Gly Ile Asn Leu Gly Glu Asn Leu	
100 105 110	
AGC ACC GAG ATA ACA GTC TCA GGG AC GGC TCC GCT GCC ATA GAG GCC	384
Ser Thr Glu Ile Thr Val Ser Gly Thr Ala Ser Ala Ala Ile Glu Ala	
115 120 125	
TCA ACT CAT GGA ATT CCG AGC ATA GCG ATT AGC CTT GAG GTG GAG TGG	432
Ser Thr His Gly Ile Pro Ser Ile Ala Ile Ser Leu Glu Val Glu Trp	
130 135 140	
AAG AAG ACC CTC GGC GAG GGT GAG GGG GTT GAC TTC TCG GTC TCG ACT	480
Lys Lys Thr Leu Gly Glu Gly Glu Gly Val Asp Phe Ser Val Ser Thr	
145 150 155 160	
CAC TTC CTC AAG AGA ATC GCG GGA GCC CTC TTG GAG AGA GGT CTT CCT	528
His Phe Leu Lys Arg Ile Ala Gly Ala Leu Leu Glu Arg Gly Leu Pro	
165 170 175	
GAG GGC GTT GAC ATG CTC AAC GTC AAC GTT CCG AGC GAC GCG ACG GAG	576
Glu Gly Val Asp Met Leu Asn Val Asn Val Pro Ser Asp Ala Thr Glu	
180 185 190	
GAA ACG GAG ATA GCA ATC ACC CGC TTA GCC CGG AAG CGC TAC TCC CCA	624
Glu Thr Glu Ile Ala Ile Thr Arg Leu Ala Arg Lys Arg Tyr Ser Pro	
195 200 205	
ACG GTC GAG GAG AGG ATT GAC CCC AAG GGC AAC CCC TAC TAC TGG ATT	672
Thr Val Glu Glu Arg Ile Asp Pro Lys Gly Asn Pro Tyr Tyr Trp Ile	
210 215 220	
GTC GGC AAA CTT GTC CAA GAC TTC GAG CCA GGG ACA GAT GCC TAC GCC	720
Val Gly Lys Leu Val Gln Asp Phe Glu Pro Gly Thr Asp Ala Tyr Ala	
225 230 235 240	
CTG AAG GTC GAG AGG AAG GTC AGC GTC ACG CCG ATA AAC ATA GAT ATG	768
Leu Lys Val Glu Arg Lys Val Ser Val Thr Pro Ile Asn Ile Asp Met	
245 250 255	
ACT GCG AGG GTG GAC TTT GAG GAG CTT GTA AGG GTT CTG TGG GTG	813
Thr Ala Arg Val Asp Phe Glu Glu Leu Val Arg Val Leu Trp Val	
260 265 270	
TAA	816

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG AAA GGA AAG TCT CTT GTT AGC GGT CTG TTG TTG GGT CTT TTA ATT	48
Met Lys Gly Lys Ser Leu Val Ser Gly Leu Leu Leu Gly Leu Leu Ile	
1 5 10 15	
TTG AGC CTG ATT TCA TTC CAG CCA AGC TTT GCA TAC TCC CCA CAC GGC	96
Leu Ser Leu Ile Ser Phe Gln Pro Ser Phe Ala Tyr Ser Pro His Gly	
20 25 30	
GGT GTC AAA AAC ATC ATA ATC CTG GTT GGA GAC GGC ATG GGT CTT GGG	144
Gly Val Lys Asn Ile Ile Ile Leu Val Gly Asp Gly Met Gly Leu Gly	
35 40 45	
CAT GTA GAA ATT ACA AAG CTC GTT TAT GGA CAC TTA AAC ATG GAA AAC	192
His Val Glu Ile Thr Lys Leu Val Tyr Gly His Leu Asn Met Glu Asn	
50 55 60	
TTT CCA GTT ACT GGA TTT GAG CTT ACT GAT TCC CTA AGT GGT GAA GTT	240
Phe Pro Val Thr Gly Phe Glu Leu Thr Asp Ser Leu Ser Gly Glu Val	
65 70 75 80	
ACA GAT TCT GCT GCG GCA GGA ACT GCA ATA TCC ACT GGA GCT AAA ACG	288
Thr Asp Ser Ala Ala Ala Gly Thr Ala Ile Ser Thr Gly Ala Lys Thr	
85 90 95	
TAT AAT GGT ATG ATT TCA GTA ACC AAC ATA ACC GGA AAG ATA GTT AAC	336
Tyr Asn Gly Met Ile Ser Val Thr Asn Ile Thr Gly Lys Ile Val Asn	
100 105 110	
TTA ACA ACC CTA CTT GAA GTG GCT CAA GAG CTT GGG AAG TCA ACA GGG	384
Leu Thr Thr Leu Leu Glu Val Ala Gln Glu Leu Gly Lys Ser Thr Gly	
115 120 125	
CTG GTC ACC ACA ACA AGG ATT ACC CAT GCA ACT CCA GCA GTT TTT GCG	432
Leu Val Thr Thr Thr Arg Ile Thr His Ala Thr Pro Ala Val Phe Ala	
130 135 140	
TCC CAT GTC CCA GAT AGG GAT ATG GAG GGG GAG ATA CCC AAG CAA CTC	480
Ser His Val Pro Asp Arg Asp Met Glu Gly Glu Ile Pro Lys Gln Leu	
145 150 155 160	
ATA ATG CAC AAA GTT AAC GTC TTG TTG GGT GGT GGA AGG GAG AAA TTC	528
Ile Met His Lys Val Asn Val Leu Leu Gly Gly Gly Arg Glu Lys Phe	
165 170 175	
GAT GAG AAA AAT TTG GAG CTG GCC AAA AAG CAG GGA TAC AAA GTA GTT	576
Asp Glu Lys Asn Leu Glu Leu Ala Lys Lys Gln Gly Tyr Lys Val Val	
180 185 190	
TTC ACG AAG GAA GAG CTT GAA AAA GTT GAA GGA GAT TAT GTC CTA GGA	624
Phe Thr Lys Glu Glu Leu Glu Lys Val Glu Gly Asp Tyr Val Leu Gly	
195 200 205	
CTC TTT GCA GAA AGT CAC ATC CCT TAC GTA TTG GAT AGA AAA CCC GAT	672
Leu Phe Ala Glu Ser His Ile Pro Tyr Val Leu Asp Arg Lys Pro Asp	
210 215 220	
GAT GTT GGA CTT TTA GAA ATG GCC AAA AAG GCA ATT TCA ATA CTC GAG	720
Asp Val Gly Leu Leu Glu Met Ala Lys Lys Ala Ile Ser Ile Leu Glu	
225 230 235 240	
AAG AAC CCG AGC GGA TTC TTT CTC ATG GTT GAG GGC GGA AGG ATT GAC	768
Lys Asn Pro Ser Gly Phe Phe Leu Met Val Glu Gly Gly Arg Ile Asp	

[illegible]

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG CCA AGA AAT ATC GCC GCT GTA TGC GCC CTG GCC GCT TTG TTA GGG	48
Met Pro Arg Asn Ile Ala Ala Val Cys Ala Leu Ala Ala Leu Leu Gly	
1 5 10 15	
TCG GCC TGG GCG GCC AAA GTT GCC GTC TAC CCC TAC GAC GGA GCC GCT	96
Ser Ala Trp Ala Ala Lys Val Ala Val Tyr Pro Tyr Asp Gly Ala Ala	
20 25 30	
TTG CTG GCG GGG CAG CGC TTC GAT TTG CGC ATA GAA GCC TCC GAG CTG	144
Leu Leu Ala Gly Gln Arg Phe Asp Leu Arg Ile Glu Ala Ser Glu Leu	
35 40 45	
AAA GGC AAT TTA AAG GCT TAC CGC ATC ACC CTG GAC GGC CAG CCT CTG	192
Lys Gly Asn Leu Lys Ala Tyr Arg Ile Thr Leu Asp Gly Gln Pro Leu	
50 55 60	
GCG GGC CTC GAG CAA ACC GCG CAG GGG GCC GGG CAG GCC GAG TGG ACC	240
Ala Gly Leu Glu Gln Thr Ala Gln Gly Ala Gly Gln Ala Glu Trp Thr	
65 70 75 80	
CTG CGC GGT GCC TTC CTG CGC CCT GGA AGC CAC ACC CTC GAG GTC AGC	288
Leu Arg Gly Ala Phe Leu Arg Pro Gly Ser His Thr Leu Glu Val Ser	
85 90 95	
CTC ACC GAC GAC GCT GGG GAG AGC AGG AAG AGC GTA CGT TGG GAG GCT	336
Leu Thr Asp Asp Ala Gly Glu Ser Arg Lys Ser Val Arg Trp Glu Ala	
100 105 110	
CGG CAG AAC CTT CGC TTG CCC CGA GCG GCC AAG AAT GTG ATT CTC TTC	384
Arg Gln Asn Leu Arg Leu Pro Arg Ala Ala Lys Asn Val Ile Leu Phe	
115 120 125	
ATT GGC GAC GGG ATG GGC TGG AAC ACC CTC AAC GCC GCC CGC ATC ATC	432
Ile Gly Asp Gly Met Gly Trp Asn Thr Leu Asn Ala Ala Arg Ile Ile	
130 135 140	
GCC AAA GGC TTT AAC CCC GAA AAC GGT ATG CCC AAC GGA AAC CTC GAG	480
Ala Lys Gly Phe Asn Pro Glu Asn Gly Met Pro Asn Gly Asn Leu Glu	
145 150 155 160	
ATC GAG AGT GGT TAC GGT GGG ATG GCT ACC GTC ACT ACC GGC AGC TTT	528
Ile Glu Ser Gly Tyr Gly Gly Met Ala Thr Val Thr Thr Gly Ser Phe	
165 170 175	
GAT AGC TTC ATC GCC GAC TCA GCT AAC TCG GCT TCT TCC ATC ATG ACC	576
Asp Ser Phe Ile Ala Asp Ser Ala Asn Ser Ala Ser Ser Ile Met Thr	
180 185 190	

GGG Gly	CAG Gln	AAG Lys	GTG Val	CAG Gln	GTG Val	AAT Asn	GCC Ala	CTC Leu	AAC Asn	GTT Val	TAC Tyr	CCA Pro	TCA Ser	AAC Asn	CTC Leu	624
		195					200					205				
AAA Lys	GAT Asp	ACC Thr	CTG Leu	GCC Ala	TAC Tyr	CCC Pro	CGG Arg	ATC Ile	GAA Glu	ACC Thr	CTA Leu	GCG Ala	GAG Glu	ATG Met	CTC Leu	672
		210				215					220					
AAG Lys	CGG Arg	GTA Val	CGC Arg	GGG Gly	GCC Ala	AGC Ser	ATT Ile	GGG Gly	GTA Val	GTG Val	ACC Thr	ACC Thr	ACC Thr	TTC Phe	GGC Gly	720
		225			230					235					240	
ACC Thr	GAC Asp	GCT Ala	ACC Thr	CCG Pro	GCT Ala	TCA Ser	CTC Leu	AAC Asn	GCC Ala	CAT His	ACC Thr	CGC Arg	CGC Arg	CGC Arg	GGT Gly	768
				245					250						255	
GAT Asp	TAC Tyr	CAG Gln	GCT Ala	ATC Ile	GCC Ala	GAC Asp	ATG Met	TAC Tyr	TTT Phe	GGT Gly	AGA Arg	GGC Gly	GGG Gly	TTC Phe	GGT Gly	816
			260					265					270			
GTT Val	CCC Pro	TTG Leu	GAT Asp	GTG Val	ATG Met	CTC Leu	TTC Phe	GGT Gly	GGT Gly	TCA Ser	CGC Arg	GAC Asp	TTC Phe	ATC Ile	CCC Pro	864
		275					280					285				
CAG Gln	AGC Ser	ACC Thr	CCT Pro	GGC Gly	TCG Ser	CGG Arg	CGC Arg	AAG Lys	GAT Asp	AGC Ser	ACG Thr	GAC Asp	TGG Trp	ATT Ile	GCC Ala	912
		290				295					300					
GAA Glu	TCC Ser	CAG Gln	AAG Lys	CTG Leu	GGC Gly	TAC Tyr	ACC Thr	TTT Phe	GTC Val	AGC Ser	ACC Thr	CGC Arg	AGC Ser	GAG Glu	CTG Leu	960
		305			310					315					320	
CTG Leu	GCG Ala	GCC Ala	AAA Lys	CCC Pro	ACC Thr	GAT Asp	AAG Lys	CTG Leu	TTT Phe	GGG Gly	CTG Leu	TTC Phe	AAC Asn	ATT Ile	GAC Asp	1008
				325					330					335		
AAC Asn	TTC Phe	CCC Pro	AGC Ser	TAC Tyr	CTA Leu	GAC Asp	CGC Arg	GCA Ala	GTG Val	TGG Trp	AAG Lys	CGG Arg	CCC Pro	GAG Glu	ATG Met	1056
			340					345					350			
CTG Leu	GGA Gly	AGC Ser	TTT Phe	ACC Thr	GAT Asp	ATG Met	CCC Pro	TAC Tyr	CTC Leu	TGG Trp	GAG Glu	ATG Met	ACC Thr	CAG Gln	AAA Lys	1104
		355					360					365				
GCC Ala	GTG Val	GAG Glu	GCT Ala	CTC Leu	TCC Ser	AGA Arg	AAC Asn	GAC Asp	AAA Lys	GGC Gly	TTT Phe	TTC Phe	TTG Leu	ATG Met	GTT Val	1152
		370				375					380					
GAG Glu	GGG Gly	GGA Gly	ATG Met	GTG Val	GAT Asp	AAG Lys	TAC Tyr	GAG Glu	CAC His	CCC Pro	TTG Leu	GAC Asp	TGG Trp	CCC Pro	CGC Arg	1200
		385			390					395				400		
GCA Ala	CTT Leu	TGG Trp	GAT Asp	GTA Val	CTC Leu	GAG Glu	CTG Leu	GAC Asp	CGC Arg	GCG Ala	GTG Val	GCT Ala	TGG Trp	GCC Ala	AAG Lys	1248
				405					410					415		
GGC Gly	TAT Tyr	GCG Ala	GCC Ala	TCC Ser	CAC His	CCC Pro	GAT Asp	ACC Thr	CTG Leu	GTG Val	ATT Ile	GTC Val	ACC Thr	GCC Ala	GAC Asp	1296
			420				425						430			
CAC His	GCT Ala	CAC His	TCG Ser	ATC Ile	TCG Ser	GTG Val	TTT Phe	GGC Gly	GGT Gly	TAC Tyr	GAC Asp	TAC Tyr	TCC Ser	AAG Lys	CAG Gln	1344
		435					440					445				
GGC Gly	CGG Arg	GAG Glu	GGG Gly	GTG Val	GGG Gly	GTT Val	TAT Tyr	GAG Glu	GCC Ala	GCC Ala	AAG Lys	TTC Phe	CCC Pro	ACC Thr	TAC Leu	1392

Gly	Arg	Glu	Gly	Val	Gly	Val	Tyr	Glu	Ala	Ala	Lys	Phe	Pro	Thr	Tyr	
450					455						460					
GGC	GAC	AAA	AAA	GAC	GCC	AAC	GGC	TTT	CCC	TTG	CCC	GAC	ACC	ACT	CGG	1440
Gly	Asp	Lys	Lys	Asp	Ala	Asn	Gly	Phe	Pro	Leu	Pro	Asp	Thr	Thr	Arg	
465					470					475					480	
GGA	ATC	GCG	GTA	GGC	TTC	GGG	GCC	ACG	CCG	GAT	TAC	TGT	GAA	ACC	TAC	1488
Gly	Ile	Ala	Val	Gly	Phe	Gly	Ala	Thr	Pro	Asp	Tyr	Cys	Glu	Thr	Tyr	
				485					490					495		
CGG	GGC	CGC	GAG	GTC	TAC	AAA	GAC	CCC	ACC	ATC	TCC	GAC	GGC	AAA	GGT	1536
Arg	Gly	Arg	Glu	Val	Tyr	Lys	Asp	Pro	Thr	Ile	Ser	Asp	Gly	Lys	Gly	
			500					505					510			
GGT	TAC	GTG	GCC	AAC	CCT	GAG	GTC	TGC	AAG	GAG	CCG	GGC	CTT	CCA	ACG	1584
Gly	Tyr	Val	Ala	Asn	Pro	Glu	Val	Cys	Lys	Glu	Pro	Gly	Leu	Pro	Thr	
		515				520						525				
TAC	CGG	CAA	CTC	CCA	GTA	GAT	AGC	GCC	CAG	GGC	GTG	CAC	ACG	GCT	GAT	1632
Tyr	Arg	Gln	Leu	Pro	Val	Asp	Ser	Ala	Gln	Gly	Val	His	Thr	Ala	Asp	
	530					535					540					
CCC	ATG	CCG	CTG	TTT	GCC	TTT	GGC	GTG	GGG	TCT	CAG	TTC	TTC	AAT	GGC	1680
Pro	Met	Pro	Leu	Phe	Ala	Phe	Gly	Val	Gly	Ser	Gln	Phe	Phe	Asn	Gly	
545					550					555					560	
CTC	ATC	GAC	CAG	ACC	GAG	ATC	TTC	TTC	CGC	ATG	GCC	CAG	GCC	CTA	GGG	1728
Leu	Ile	Asp	Gln	Thr	Glu	Ile	Phe	Phe	Arg	Met	Ala	Gln	Ala	Leu	Gly	
				565					570					575		
TTC	AAC	CCC	CAC	CTC	GAG	AAG	CCT	TAA								1755
Phe	Asn	Pro	His	Leu	Glu	Lys	Pro									
			580													

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG	TAT	AAA	TGG	ATT	ATT	GAG	GGT	AAG	CTT	GCC	CAA	GCA	CCT	TTT	CCA	48
Met	Tyr	Lys	Trp	Ile	Ile	Glu	Gly	Lys	Leu	Ala	Gln	Ala	Pro	Phe	Pro	
1				5					10					15		
AGC	CTA	GGT	GAA	CTA	GCC	GAT	CTC	AAA	AGA	CTT	TTC	GAC	GCC	ATT	ATT	96
Ser	Leu	Gly	Glu	Leu	Ala	Asp	Leu	Lys	Arg	Leu	Phe	Asp	Ala	Ile	Ile	
			20					25					30			
GTT	CTT	ACA	ATG	CCG	CAT	GAA	CAA	CCG	CTT	AAT	GAG	AAA	TAT	ATC	GAG	144
Val	Leu	Thr	Met	Pro	His	Glu	Gln	Pro	Leu	Asn	Glu	Lys	Tyr	Ile	Glu	
			35					40				45				
ATA	TTA	GAG	AGC	CAT	GGA	TTC	CAA	GTC	CTC	CAT	GTC	CCC	ACG	CTC	GAC	192
Ile	Leu	Glu	Ser	His	Gly	Phe	Gln	Val	Leu	His	Val	Pro	Thr	Leu	Asp	

50	55	60	
TTT CAT CCT TTA GAA CTC TTC GAC CTT TTG AAA ACA AGC ATA TTC ATT Phe His Pro Leu Glu Leu Phe Asp Leu Leu Lys Thr Ser Ile Phe Ile 65 70 75 80	240		
GAT GAA AAC CTG GAG AGA TCC CAC AGA GTG CTT GTC CAC TGC ATG GGA Asp Glu Asn Leu Glu Arg Ser His Arg Val Leu Val His Cys Met Gly 85 90 95	288		
GGC ATA GGC CGG AGC GGG CTT GTA ACT GCT GCG TAC TTA ATA TTC AAA Gly Ile Gly Arg Ser Gly Leu Val Thr Ala Ala Tyr Leu Ile Phe Lys 100 105 110	336		
GGT TAT GAT ATT TAC GAC GCG GTA AAG CAT GTG AGA ACG GTA GTG CCT Gly Tyr Asp Ile Tyr Asp Ala Val Lys His Val Arg Thr Val Val Pro 115 120 125	384		
GGT GCT ATT GAA AAC AGA GGG CAA GCG TTA ATG CTT GAG AAC TAC TAT Gly Ala Ile Glu Asn Arg Gly Gln Ala Leu Met Leu Glu Asn Tyr Tyr 130 135 140	432		
ACC CTG GTC AAA AGT TTC AAC AGA GAG TTG CTG AGA GAC TAC GGG AAG Thr Leu Val Lys Ser Phe Asn Arg Glu Leu Arg Asp Tyr Gly Lys 145 150 155 160	480		
AAA ATT TTC ACG CTC GGT GAC CCG AAG GCG GTT CTC CAC GCT TCT AAG Lys Ile Phe Thr Leu Gly Asp Pro Lys Ala Val Leu His Ala Ser Lys 165 170 175	528		
ACG ACT CAG TTC ACG ATT GAA CTC TTA AGC AAC TTA CAC GTC AAC GAG Thr Thr Gln Phe Thr Ile Glu Leu Leu Ser Asn Leu His Val Asn Glu 180 185 190	576		
GCG TTT TCA ATC AGT GCG ATG GCT CAA TCA CTG CTC CAC TTT CAC GAC Ala Phe Ser Ile Ser Ala Met Ala Gln Ser Leu Leu His Phe His Asp 195 200 205	624		
GTA AAA GTC CGC TCT AAA CTG AAA GAA GTA TTC GAA AAC ATG GAA TTC Val Lys Val Arg Ser Lys Leu Lys Glu Val Phe Glu Asn Met Glu Phe 210 215 220	672		
TCA TCC GCC TCA GAG GAG GTT CTG TCA TTT ATT CAC CTA CTC GAT TTC Ser Ser Ala Ser Glu Glu Val Leu Ser Phe Ile His Leu Leu Asp Phe 225 230 235 240	720		
TAT CAG GAT GGC AGG GTT GTT TTA ACC ATT TAC GAT TAT CTC CCC GAT Tyr Gln Asp Gly Arg Val Val Leu Thr Ile Tyr Asp Tyr Leu Pro Asp 245 250 255	768		
AGG GTG GAT TTG ATT TTA TTG TGT AAG TGG GGT TGT GAT AAA ATA GTT Arg Val Asp Leu Ile Leu Leu Cys Lys Trp Gly Cys Asp Lys Ile Val 260 265 270	816		
GAA GTC TCG TCT TCA GCG AAG AAA ACC GTT GAG AAG CTT GTA GGA AGA Glu Val Ser Ser Ser Ala Lys Lys Thr Val Glu Lys Leu Val Gly Arg 275 280 285	864		
AAG GTT TCC CTA TCC TGG GCT AAT TAC TTA GAC TAT GTT TAG Lys Val Ser Leu Ser Trp Ala Asn Tyr Leu Asp Tyr Val 290 295 300	906		

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG AGA ATC CTC CTC ACC AAC GAC GAC GGC ATC TAT TCC AAC GGT CTG	48
Met Arg Ile Leu Leu Thr Asn Asp Asp Gly Ile Tyr Ser Asn Gly Leu	
1 5 10 15	
CGC GCG GCG GTG AAG GGC CTG AGC GAG CTC GGC GAG GTC TAC GTC GTC	96
Arg Ala Ala Val Lys Gly Leu Ser Glu Leu Gly Glu Val Tyr Val Val	
20 25 30	
GCC CCG CTC TTC CAG AGG AGC GCG AGC GGT CGG GCG ATG ACC CTA CAC	144
Ala Pro Leu Phe Gln Arg Ser Ala Ser Gly Arg Ala Met Thr Leu His	
35 40 45	
AGG CCG ATA AGG GCA AAG AGG GTT GAC GTT CCC GGC GCG AAG ATA GCG	192
Arg Pro Ile Arg Ala Lys Arg Val Asp Val Pro Gly Ala Lys Ile Ala	
50 55 60	
TAT GGC ATA GAC GGA ACG CCG ACC GAC TGC GTG ATT TTT GCC ATC GCC	240
Tyr Gly Ile Asp Gly Thr Pro Thr Asp Cys Val Ile Phe Ala Ile Ala	
65 70 75 80	
CGC TTC GGC GAC TTT GAT CTG GCG GTC AGC GGG ATA AAC CTA GGC GAG	288
Arg Phe Gly Asp Phe Asp Leu Ala Val Ser Gly Ile Asn Leu Gly Glu	
85 90 95	
AAC CTG AGC ACG GAG ATA ACC GTC TCC GGA ACG GCC TCG GCG GCG ATA	336
Asn Leu Ser Thr Glu Ile Thr Val Ser Gly Thr Ala Ser Ala Ala Ile	
100 105 110	
GAG GCT TCC ACC CAC GGG ATT CCA AGT GTA GCT ATA AGC CTC GAG GTC	384
Glu Ala Ser Thr His Gly Ile Pro Ser Val Ala Ile Ser Leu Glu Val	
115 120 125	
GAG TGG AAG AAG ACC CTC GGC GAG GGG GAG GGT ATT GAC TTC TCG GTT	432
Glu Trp Lys Lys Thr Leu Gly Glu Gly Glu Gly Ile Asp Phe Ser Val	
130 135 140	
TCA GCA CAC TTC CTG AGA AGG ATA GCG ACG GCT GTC CTT AAG AAG GGC	480
Ser Ala His Phe Leu Arg Arg Ile Ala Thr Ala Val Leu Lys Lys Gly	
145 150 155 160	
CTG CCT GAA GGG GTG GAC ATG CTC AAC GTG AAC GTC CCT AGC GAC GCC	528
Leu Pro Glu Gly Val Asp Met Leu Asn Val Asn Val Pro Ser Asp Ala	
165 170 175	
AGC GAG GGG ACT GAG ATC GCC ATA ACG CGC CTC GCG AGG AAG CGC TAT	576
Ser Glu Gly Thr Glu Ile Ala Ile Thr Arg Leu Ala Arg Lys Arg Tyr	
180 185 190	
TCT CCG ACG ATA GAG GAG AGG ATA GAC CCC AAG GGC AAC CCC TAC TAC	624
Ser Pro Thr Ile Glu Glu Arg Ile Asp Pro Lys Gly Asn Pro Tyr Tyr	
195 200 205	

TGG ATC GTT GGC AGG CTC GTC CAG GAG TTC GAG CCG GGC ACG GAC GCC	672
Trp Ile Val Gly Arg Leu Val Gln Glu Phe Glu Pro Gly Thr Asp Ala	
210 215 220	
TAC GCT CTG AAA GTC GAG AGA AAG GTC AGC GTC ACG CCC ATA AAC ATC	720
Tyr Ala Leu Lys Val Glu Arg Lys Val Ser Val Thr Pro Ile Asn Ile	
225 230 235 240	
GAC ATG ACT GCG AGG GTT GAC TTT GAG AAC CTT CAA AGG CTT CTG AGC	768
Asp Met Thr Ala Arg Val Asp Phe Glu Asn Leu Gln Arg Leu Leu Ser	
245 250 255	
CTG TGA	774
Leu	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG GAA AAC TTA AAA AAG TAC CTA GAA GTT GCA AAA ATA GCC GCG CTC	48
Met Glu Asn Leu Lys Lys Tyr Leu Glu Val Ala Lys Ile Ala Ala Leu	
1 5 10 15	
GCG GGT GGG CAG GTT CTG AAA GAA AAC TTC GGA AAG GTA AAA AAG GAA	96
Ala Gly Gly Gln Val Leu Lys Glu Asn Phe Gly Lys Val Lys Lys Glu	
20 25 30	
AAC ATA GAG GAA AAA GGG GAA AAG GAC TTT GTA AGT TAC GTG GAT AAA	144
Asn Ile Glu Glu Lys Gly Glu Lys Asp Phe Val Ser Tyr Val Asp Lys	
35 40 45	
ACT TCA GAG GAA AGG ATA AAG GAG GTG ATA CTC AAG TTC TTT CCC GAT	192
Thr Ser Glu Glu Arg Ile Lys Glu Val Ile Leu Lys Phe Phe Pro Asp	
50 55 60	
CAC GAG GTC GTA GGG GAA GAG ATG GGT GCG GAG GGA AGC GGA AGC GAA	240
His Glu Val Val Gly Glu Glu Met Gly Ala Glu Gly Ser Gly Ser Glu	
65 70 75 80	
TAC AGG TGG TTC ATA GAC CCC CTT GAC GGC ACA AAG AAC TAC ATA AAC	288
Tyr Arg Trp Phe Ile Asp Pro Leu Asp Gly Thr Lys Asn Tyr Ile Asn	
85 90 95	
GGT TTT CCC ATC TTT GCC GTA TCA GTG GGA CTT GTT AAG GGA GAA GAG	336
Gly Phe Pro Ile Phe Ala Val Ser Val Gly Leu Val Lys Gly Glu Glu	
100 105 110	
CCA ATT GTG GGT GCG GTT TAC CTT CCT TAC TTT GAC AAG CTT TAC TGG	384
Pro Ile Val Gly Ala Val Tyr Leu Pro Tyr Phe Asp Lys Leu Tyr Trp	
115 120 125	
GGT GCT AAA GGT CTC GGG GCT TAC GTA AAC GGA AAG AGG ATA AAG GTA	432

Gly	Ala	Lys	Gly	Leu	Gly	Ala	Tyr	Val	Asn	Gly	Lys	Arg	Ile	Lys	Val		
130						135					140						
AAG	GAC	AAT	GAG	AGT	TTA	AAG	CAC	GCC	GGA	GTG	GTT	TAC	GGA	TTT	CCC	480	
Lys	Asp	Asn	Glu	Ser	Leu	Lys	His	Ala	Gly	Val	Val	Tyr	Gly	Phe	Pro	145	160
					150					155							
TCT	AGG	AGC	AGG	AGG	GAC	ATA	TCT	ATC	TAC	TTG	AAC	ATA	TTC	AAG	GAT	528	
Ser	Arg	Ser	Arg	Arg	Asp	Ile	Ser	Ile	Tyr	Leu	Asn	Ile	Phe	Lys	Asp		
				165					170					175			
GTC	TTT	TAC	GAA	GTT	GGC	TCT	ATG	AGG	AGA	CCC	GGG	GCT	GCT	GCG	GTT	576	
Val	Phe	Tyr	Glu	Val	Gly	Ser	Met	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Val		
			180					185					190				
GAC	CTC	TGC	ATG	GTG	GCG	GAA	GGG	ATA	TTT	GAC	GGG	ATG	ATG	GAG	TTT	624	
Asp	Leu	Cys	Met	Val	Ala	Glu	Gly	Ile	Phe	Asp	Gly	Met	Met	Glu	Phe		
			195				200					205					
GAA	ATG	AAG	CCG	TGG	GAC	ATA	ACC	GCA	GGG	CTT	GTA	ATA	CTG	AAG	GAA	672	
Glu	Met	Lys	Pro	Trp	Asp	Ile	Thr	Ala	Gly	Leu	Val	Ile	Leu	Lys	Glu		
	210					215					220						
GCC	GGG	GGC	GTT	TAC	ACA	CTT	GTG	GGA	GAA	CCC	TTC	GGA	GTT	TCG	GAC	720	
Ala	Gly	Gly	Val	Tyr	Thr	Leu	Val	Gly	Glu	Pro	Phe	Gly	Val	Ser	Asp		
	225					230				235					240		
ATA	ATT	GCG	GGC	AAC	AAA	GCC	CTC	CAC	GAC	TTT	ATA	CTT	CAG	GTA	GCC	768	
Ile	Ile	Ala	Gly	Asn	Lys	Ala	Leu	His	Asp	Phe	Ile	Leu	Gln	Val	Ala		
				245					250					255			
AAA	AAG	TAT	ATG	GAA	GTG	GCG	GTG	TGA								795	
Lys	Lys	Tyr	Met	Glu	Val	Ala	Val										
			260														

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Arg	Gly	Ser	Gly	Val	Arg	Ile	Leu	Leu	Thr	Asn	Asp	Asp	Gly	Ile		
1				5				10						15			
Phe	Ala	Glu	Gly	Leu	Gly	Ala	Leu	Arg	Lys	Met	Leu	Glu	Pro	Val	Ala		
		20						25					30				
Thr	Leu	Tyr	Val	Val	Ala	Pro	Asp	Arg	Glu	Arg	Ser	Ala	Ala	Ser	His		
		35					40					45					
Ala	Ile	Thr	Val	His	Arg	Pro	Leu	Arg	Val	Arg	Glu	Ala	Gly	Phe	Arg		
	50				55					60							
Ser	Pro	Arg	Leu	Lys	Gly	Trp	Val	Val	Asp	Gly	Thr	Pro	Ala	Asp	Cys		
	65			70					75					80			
Val	Lys	Leu	Gly	Leu	Glu	Val	Leu	Leu	Pro	Glu	Arg	Pro	Asp	Phe	Leu		
			85				90						95				
Val	Ser	Gly	Ile	Asn	Tyr	Gly	Pro	Asn	Leu	Gly	Thr	Asp	Val	Leu	Tyr		
		100					105					110					
Ser	Gly	Thr	Val	Ser	Ala	Ala	Ile	Glu	Gly	Val	Ile	Asn	Gly	Ile	Pro		
	115						120					125					
Ser	Val	Ala	Val	Ser	Leu	Ala	Thr	Arg	Arg	Glu	Pro	Asp	Tyr	Thr	Trp		

130	Ala	Ala	Arg	Phe	Val	Leu	Val	Leu	Leu	Glu	Glu	Leu	Arg	Lys	His	Gln
145	Leu	Pro	Pro	Gly	Thr	Leu	Leu	Asn	Val	Asn	Val	Pro	Asp	Gly	Val	Pro
	Arg	Gly	Val	Lys	Val	Thr	Lys	Leu	Gly	Ser	Val	Arg	Tyr	Val	Asn	Val
	Val	Asp	Cys	Arg	Thr	Asp	Pro	Arg	Gly	Lys	Ala	Tyr	Tyr	Trp	Met	Ala
	Gly	Glu	Pro	Leu	Glu	Leu	Asp	Gly	Asn	Asp	Ser	Glu	Thr	Asp	Val	Trp
	Ala	Val	Arg	Glu	Gly	Tyr	Ile	Ser	Val	Thr	Pro	Val	Gln	Ile	Asp	Leu
	Thr	Asn	Tyr	Gly	Phe	Leu	Glu	Glu	Leu	Lys	Lys	Trp	Arg	Phe	Lys	Asp
	Ile	Phe	Ser	Ser												

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Leu	Asp	Ile	Leu	Leu	Val	Asn	Asp	Asp	Gly	Ile	Tyr	Ser	Asn	Gly
1				5					10					15	
Leu	Ile	Ala	Leu	Lys	Asp	Ala	Leu	Leu	Glu	Lys	Phe	Asn	Ala	Arg	Ile
			20					25					30		
Thr	Ile	Val	Ala	Pro	Thr	Asn	Gln	Gln	Ser	Gly	Ile	Gly	Arg	Ala	Ile
		35				40					45				
Ser	Leu	Phe	Glu	Pro	Leu	Arg	Ile	Thr	Lys	Thr	Lys	Leu	Ala	Asp	Gly
	50				55					60					
Ser	Trp	Gly	Tyr	Ala	Val	Ser	Gly	Thr	Pro	Thr	Asp	Cys	Val	Ile	Leu
	65				70				75					80	
Gly	Ile	Tyr	Glu	Ile	Leu	Lys	Lys	Val	Pro	Asp	Val	Val	Ile	Ser	Gly
			85					90					95		
Ile	Asn	Ile	Gly	Asn	Leu	Gly	Thr	Glu	Ile	Thr	Thr	Ser	Gly	Thr	
		100					105					110			
Leu	Gly	Ala	Ala	Phe	Glu	Gly	Ala	His	His	Gly	Ala	Lys	Ala	Leu	Ala
	115					120					125				
Ser	Ser	Leu	Gln	Val	Thr	Ser	Asp	His	Leu	Lys	Phe	Lys	Glu	Gly	Glu
	130				135				140						
Thr	Pro	Ile	Asp	Phe	Thr	Val	Pro	Ala	Arg	Ile	Thr	Ala	Asn	Val	Val
	145			150					155					160	
Glu	Lys	Met	Leu	Asp	Tyr	Asp	Phe	Pro	Cys	Asp	Val	Val	Asn	Leu	Asn
			165					170					175		
Ile	Pro	Glu	Gly	Ala	Thr	Glu	Lys	Thr	Pro	Ile	Glu	Ile	Thr	Arg	Leu
		180					185				190				
Ala	Arg	Lys	Met	Tyr	Thr	Thr	His	Val	Glu	Glu	Arg	Ile	Asp	Pro	Arg
	195					200					205				
Gly	Arg	Ser	Tyr	Tyr	Trp	Ile	Asp	Gly	Tyr	Pro	Ile	Leu	Glu	Glu	Glu
	210				215					220					
Glu	Asp	Thr	Asp	Val	Tyr	Val	Val	Arg	Arg	Lys	Gly	His	Ile	Ser	Leu
	225				230				235					240	
Thr	Pro	Leu	Thr	Leu	Asp	Thr	Thr	Ile	Lys	Asn	Leu	Glu	Glu	Phe	Lys
			245					250					255		
Lys	Lys	Tyr	Glu	Arg	Ile	Leu	Asn	Glu							
			260					265							

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Met	Met	Glu	Phe	Thr	Arg	Glu	Gly	Ile	Lys	Ala	Ala	Val	Glu	Ala	
1				5					10					15		
Leu	Gln	Gly	Leu	Gly	Glu	Ile	Tyr	Val	Val	Ala	Pro	Met	Phe	Gln	Arg	
			20					25					30			
Ser	Ala	Ser	Gly	Arg	Ala	Met	Thr	Ile	His	Arg	Pro	Leu	Arg	Ala	Lys	
			35				40					45				
Arg	Ile	Ser	Met	Asn	Gly	Ala	Lys	Ala	Ala	Tyr	Ala	Leu	Asp	Gly	Met	
			50			55					60					
Pro	Val	Asp	Cys	Val	Ile	Phe	Ala	Met	Ala	Arg	Phe	Gly	Asp	Phe	Asp	
					70					75					80	
Leu	Ala	Ile	Ser	Gly	Val	Asn	Leu	Gly	Glu	Asn	Met	Ser	Thr	Glu	Ile	
				85					90					95		
Thr	Val	Ser	Gly	Thr	Ala	Ser	Ala	Ala	Ile	Glu	Ala	Ala	Thr	Gln	Glu	
			100					105					110			
Ile	Pro	Ser	Ile	Pro	Ile	Ser	Leu	Glu	Val	Asn	Arg	Glu	Lys	His	Lys	
			115				120					125				
Phe	Gly	Glu	Gly	Glu	Glu	Ile	Asp	Phe	Ser	Ala	Ala	Lys	Tyr	Phe	Leu	
			130			135				140						
Arg	Lys	Ile	Ala	Thr	Ala	Val	Leu	Lys	Arg	Gly	Leu	Pro	Lys	Gly	Val	
					150					155					160	
Asp	Met	Leu	Asn	Val	Asn	Val	Pro	Tyr	Asp	Ala	Asn	Glu	Arg	Thr	Glu	
				165					170					175		
Ile	Ala	Phe	Thr	Arg	Leu	Ala	Arg	Arg	Met	Tyr	Arg	Pro	Ser	Ile	Glu	
			180				185						190			
Glu	Arg	Ile	Asp	Pro	Lys	Gly	Asn	Pro	Tyr	Tyr	Trp	Ile	Val	Gly	Thr	
			195				200					205				
Gln	Cys	Pro	Lys	Glu	Ala	Leu	Glu	Pro	Gly	Thr	Asp	Met	Tyr	Val	Val	
			210			215					220					
Lys	Val	Glu	Arg	Lys	Val	Ser	Val	Thr	Pro	Ile	Asn	Ile	Asp	Met	Thr	
					230					235					240	
Ala	Arg	Val	Asn	Leu	Asp	Glu	Ile	Lys	Arg	Leu	Leu	Glu	Leu			
				245					250							

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Arg	Thr	Leu	Thr	Ile	Asn	Thr	Asp	Ala	Glu	Gly	Phe	Val	Leu	Arg	
1				5					10					15		
Ile	Leu	Leu	Thr	Asn	Asp	Asp	Gly	Ile	Tyr	Ser	Asn	Gly	Leu	Arg	Ala	
			20					25					30			
Ala	Val	Lys	Ala	Leu	Ser	Glu	Leu	Gly	Glu	Val	Tyr	Val	Val	Ala	Pro	



Asp	Glu	Lys	Asn	Leu	Glu	Leu	Ala	Lys	Lys	Gln	Gly	Tyr	Lys	Val	Val	
			180					185					190			
Phe	Thr	Lys	Glu	Glu	Leu	Glu	Lys	Val	Glu	Gly	Asp	Tyr	Val	Leu	Gly	
		195					200					205				
Leu	Phe	Ala	Glu	Ser	His	Ile	Pro	Tyr	Val	Leu	Asp	Arg	Lys	Pro	Asp	
	210					215					220					
Asp	Val	Gly	Leu	Leu	Glu	Met	Ala	Lys	Lys	Ala	Ile	Ser	Ile	Leu	Glu	
225					230					235					240	
Lys	Asn	Pro	Ser	Gly	Phe	Phe	Leu	Met	Val	Glu	Gly	Gly	Arg	Ile	Asp	
				245					250					255		
His	Ala	Ala	His	Gly	Asn	Asp	Val	Ala	Ser	Val	Val	Ala	Glu	Thr	Lys	
			260					265					270			
Glu	Phe	Asp	Asp	Val	Val	Arg	Tyr	Val	Leu	Glu	Tyr	Pro	Lys	Lys	Arg	
		275					280					285				
Gly	Asp	Thr	Leu	Val	Ile	Val	Leu	Ala	Asp	His	Glu	Thr	Gly	Gly	Leu	
	290					295					300					
Ala	Ile	Gly	Leu	Thr	Tyr	Gly	Asn	Ala	Ile	Asp	Glu	Asp	Ala	Ile	Arg	
305					310					315					320	
Lys	Ile	Lys	Ala	Ser	Thr	Leu	Arg	Met	Pro	Lys	Glu	Val	Lys	Ala	Gly	
			325						330					335		
Ser	Ser	Val	Lys	Glu	Ser	Ser	Lys	Val	Cys	Arg	Ile	Cys	Pro	Asn	Arg	
		340						345					350			
Gly	Arg	Ser	Gln	Tyr	Ile	Glu	Asn	Ala	Leu	His	Ser	Thr	Asn	Lys	Tyr	
		355					360					365				
Ala	Leu	Ser	Asn	Ala	Val	Ala	Asp	Val	Ile	Asn	Arg	Arg	Ile	Gly	Val	
	370					375					380					
Gly	Phe	Thr	Ser	Tyr	Glu	His	Thr	Gly	Val	Pro	Val	Pro	Leu	Leu	Ala	
385					390					395					400	
Tyr	Gly	Pro	Gly	Ala	Glu	Asn	Phe	Arg	Gly	Phe	Leu	His	His	Val	Asp	
			405						410					415		
Thr	Ala	Arg	Leu	Val	Ala	Lys	Leu	Met	Leu	Phe	Gly	Arg	Arg	Asn	Ile	
			420					425					430			
Pro	Val	Thr	Ile	Ser	Ser	Val	Ser	Ser	Val	Lys	Gly	Asp	Ile	Thr	Gly	
		435					440					445				
Asp	Tyr	Arg	Val	Asp	Glu	Lys	Asp	Ala	Tyr	Val	Thr	Leu	Met	Met	Phe	
	450					455					460					
Leu	Gly	Glu	Lys	Val	Asp	Asn	Glu	Ile	Glu	Lys	Arg	Val	Asp	Ile	Asp	
465					470					475					480	
Asn	Asn	Gly	Met	Val	Asp	Leu	Asn	Asp	Val	Met	Leu	Ile	Leu	Gln	Glu	
				485					490					495		
Ala																

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Pro	Arg	Asn	Ile	Ala	Ala	Val	Cys	Ala	Leu	Ala	Ala	Leu	Leu	Gly	
1				5					10				15			
Ser	Ala	Trp	Ala	Ala	Lys	Val	Ala	Val	Tyr	Pro	Tyr	Asp	Gly	Ala	Ala	
		20					25					30				
Leu	Leu	Ala	Gly	Gln	Arg	Phe	Asp	Leu	Arg	Ile	Glu	Ala	Ser	Glu	Leu	
		35					40					45				
Lys	Gly	Asn	Leu	Lys	Ala	Tyr	Arg	Ile	Thr	Leu	Asp	Gly	Gln	Pro	Leu	
	50					55				60						
Ala	Gly	Leu	Glu	Gln	Thr	Ala	Gln	Gly	Ala	Gly	Gln	Ala	Glu	Trp	Thr	

65						70						75						80
Leu	Arg	Gly	Ala	Phe	Leu	Arg	Pro	Gly	Ser	His	Thr	Leu	Glu	Val	Ser			
				85					90					95				
Leu	Thr	Asp	Asp	Ala	Gly	Glu	Ser	Arg	Lys	Ser	Val	Arg	Trp	Glu	Ala			
			100					105					110					
Arg	Gln	Asn	Leu	Arg	Leu	Pro	Arg	Ala	Ala	Lys	Asn	Val	Ile	Leu	Phe			
		115					120					125						
Ile	Gly	Asp	Gly	Met	Gly	Trp	Asn	Thr	Leu	Asn	Ala	Ala	Arg	Ile	Ile			
	130					135					140							
Ala	Lys	Gly	Phe	Asn	Pro	Glu	Asn	Gly	Met	Pro	Asn	Gly	Asn	Leu	Glu			
	145				150					155					160			
Ile	Glu	Ser	Gly	Tyr	Gly	Gly	Met	Ala	Thr	Val	Thr	Thr	Gly	Ser	Phe			
				165					170					175				
Asp	Ser	Phe	Ile	Ala	Asp	Ser	Ala	Asn	Ser	Ala	Ser	Ser	Ile	Met	Thr			
			180					185					190					
Gly	Gln	Lys	Val	Gln	Val	Asn	Ala	Leu	Asn	Val	Tyr	Pro	Ser	Asn	Leu			
		195					200					205						
Lys	Asp	Thr	Leu	Ala	Tyr	Pro	Arg	Ile	Glu	Thr	Leu	Ala	Glu	Met	Leu			
	210					215					220							
Lys	Arg	Val	Arg	Gly	Ala	Ser	Ile	Gly	Val	Val	Thr	Thr	Thr	Phe	Gly			
	225				230					235					240			
Thr	Asp	Ala	Thr	Pro	Ala	Ser	Leu	Asn	Ala	His	Thr	Arg	Arg	Arg	Gly			
				245					250					255				
Asp	Tyr	Gln	Ala	Ile	Ala	Asp	Met	Tyr	Phe	Gly	Arg	Gly	Gly	Phe	Gly			
			260					265					270					
Val	Pro	Leu	Asp	Val	Met	Leu	Phe	Gly	Gly	Ser	Arg	Asp	Phe	Ile	Pro			
		275					280					285						
Gln	Ser	Thr	Pro	Gly	Ser	Arg	Arg	Lys	Asp	Ser	Thr	Asp	Trp	Ile	Ala			
	290					295					300							
Glu	Ser	Gln	Lys	Leu	Gly	Tyr	Thr	Phe	Val	Ser	Thr	Arg	Ser	Glu	Leu			
	305				310					315					320			
Leu	Ala	Ala	Lys	Pro	Thr	Asp	Lys	Leu	Phe	Gly	Leu	Phe	Asn	Ile	Asp			
			325						330					335				
Asn	Phe	Pro	Ser	Tyr	Leu	Asp	Arg	Ala	Val	Trp	Lys	Arg	Pro	Glu	Met			
			340					345					350					
Leu	Gly	Ser	Phe	Thr	Asp	Met	Pro	Tyr	Leu	Trp	Glu	Met	Thr	Gln	Lys			
		355					360					365						
Ala	Val	Glu	Ala	Leu	Ser	Arg	Asn	Asp	Lys	Gly	Phe	Phe	Leu	Met	Val			
	370					375					380							
Glu	Gly	Gly	Met	Val	Asp	Lys	Tyr	Glu	His	Pro	Leu	Asp	Trp	Pro	Arg			
	385				390					395					400			
Ala	Leu	Trp	Asp	Val	Leu	Glu	Leu	Asp	Arg	Ala	Val	Ala	Trp	Ala	Lys			
				405					410					415				
Gly	Tyr	Ala	Ala	Ser	His	Pro	Asp	Thr	Leu	Val	Ile	Val	Thr	Ala	Asp			
			420															

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Tyr	Lys	Trp	Ile	Ile	Glu	Gly	Lys	Leu	Ala	Gln	Ala	Pro	Phe	Pro
1				5					10					15	
Ser	Leu	Gly	Glu	Leu	Ala	Asp	Leu	Lys	Arg	Leu	Phe	Asp	Ala	Ile	Ile
			20					25					30		
Val	Leu	Thr	Met	Pro	His	Glu	Gln	Pro	Leu	Asn	Glu	Lys	Tyr	Ile	Glu
		35					40					45			
Ile	Leu	Glu	Ser	His	Gly	Phe	Gln	Val	Leu	His	Val	Pro	Thr	Leu	Asp
	50					55					60				
Phe	His	Pro	Leu	Glu	Leu	Phe	Asp	Leu	Leu	Lys	Thr	Ser	Ile	Phe	Ile
65					70					75					80
Asp	Glu	Asn	Leu	Glu	Arg	Ser	His	Arg	Val	Leu	Val	His	Cys	Met	Gly
			85						90					95	
Gly	Ile	Gly	Arg	Ser	Gly	Leu	Val	Thr	Ala	Ala	Tyr	Leu	Ile	Phe	Lys
			100					105					110		
Gly	Tyr	Asp	Ile	Tyr	Asp	Ala	Val	Lys	His	Val	Arg	Thr	Val	Val	Pro
		115					120					125			
Gly	Ala	Ile	Glu	Asn	Arg	Gly	Gln	Ala	Leu	Met	Leu	Glu	Asn	Tyr	Tyr
	130					135					140				
Thr	Leu	Val	Lys	Ser	Phe	Asn	Arg	Glu	Leu	Leu	Arg	Asp	Tyr	Gly	Lys
145					150					155					160
Lys	Ile	Phe	Thr	Leu	Gly	Asp	Pro	Lys	Ala	Val	Leu	His	Ala	Ser	Lys
			165						170					175	
Thr	Thr	Gln	Phe	Thr	Ile	Glu	Leu	Leu	Ser	Asn	Leu	His	Val	Asn	Glu
		180					185						190		
Ala	Phe	Ser	Ile	Ser	Ala	Met	Ala	Gln	Ser	Leu	Leu	His	Phe	His	Asp
		195				200						205			
Val	Lys	Val	Arg	Ser	Lys	Leu	Lys	Glu	Val	Phe	Glu	Asn	Met	Glu	Phe
	210					215					220				
Ser	Ser	Ala	Ser	Glu	Glu	Val	Leu	Ser	Phe	Ile	His	Leu	Leu	Asp	Phe
225				230					235					240	
Tyr	Gln	Asp	Gly	Arg	Val	Val	Leu	Thr	Ile	Tyr	Asp	Tyr	Leu	Pro	Asp
			245						250					255	
Arg	Val	Asp	Leu	Ile	Leu	Leu	Cys	Lys	Trp	Gly	Cys	Asp	Lys	Ile	Val
		260					265						270		
Glu	Val	Ser	Ser	Ser	Ala	Lys	Lys	Thr	Val	Glu	Lys	Leu	Val	Gly	Arg
		275				280						285			
Lys	Val	Ser	Leu	Ser	Trp	Ala	Asn	Tyr	Leu	Asp	Tyr	Val			
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Arg	Ile	Leu	Leu	Thr	Asn	Asp	Asp	Gly	Ile	Tyr	Ser	Asn	Gly	Leu
1				5					10					15	
Arg	Ala	Ala	Val	Lys	Gly	Leu	Ser	Glu	Leu	Gly	Glu	Val	Tyr	Val	Val
			20					25					30		
Ala	Pro	Leu	Phe	Gln	Arg	Ser	Ala	Ser	Gly	Arg	Ala	Met	Thr	Leu	His
		35					40					45			
Arg	Pro	Ile	Arg	Ala	Lys	Arg	Val	Asp	Val	Pro	Gly	Ala	Lys	Ile	Ala
		50				55					60				
Tyr	Gly	Ile	Asp	Gly	Thr	Pro	Thr	Asp	Cys	Val	Ile	Phe	Ala	Ile	Ala
		65			70					75					80
Arg	Phe	Gly	Asp	Phe	Asp	Leu	Ala	Val	Ser	Gly	Ile	Asn	Leu	Gly	Glu
				85					90					95	
Asn	Leu	Ser	Thr	Glu	Ile	Thr	Val	Ser	Gly	Thr	Ala	Ser	Ala	Ala	Ile
			100					105					110		
Glu	Ala	Ser	Thr	His	Gly	Ile	Pro	Ser	Val	Ala	Ile	Ser	Leu	Glu	Val
		115					120					125			
Glu	Trp	Lys	Lys	Thr	Leu	Gly	Glu	Gly	Glu	Gly	Ile	Asp	Phe	Ser	Val
	130					135					140				
Ser	Ala	His	Phe	Leu	Arg	Arg	Ile	Ala	Thr	Ala	Val	Leu	Lys	Lys	Gly
	145				150					155					160
Leu	Pro	Glu	Gly	Val	Asp	Met	Leu	Asn	Val	Asn	Val	Pro	Ser	Asp	Ala
				165				170						175	
Ser	Glu	Gly	Thr	Glu	Ile	Ala	Ile	Thr	Arg	Leu	Ala	Arg	Lys	Arg	Tyr
			180					185					190		
Ser	Pro	Thr	Ile	Glu	Glu	Arg	Ile	Asp	Pro	Lys	Gly	Asn	Pro	Tyr	Tyr
		195					200					205			
Trp	Ile	Val	Gly	Arg	Leu	Val	Gln	Glu	Phe	Glu	Pro	Gly	Thr	Asp	Ala
	210					215						220			
Tyr	Ala	Leu	Lys	Val	Glu	Arg	Lys	Val	Ser	Val	Thr	Pro	Ile	Asn	Ile
	225				230					235					240
Asp	Met	Thr	Ala	Arg	Val	Asp	Phe	Glu	Asn	Leu	Gln	Arg	Leu	Leu	Ser
				245					250					255	

Leu

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Glu	Asn	Leu	Lys	Lys	Tyr	Leu	Glu	Val	Ala	Lys	Ile	Ala	Ala	Leu
1				5					10					15	
Ala	Gly	Gly	Gln	Val	Leu	Lys	Glu	Asn	Phe	Gly	Lys	Val	Lys	Lys	Glu
			20					25					30		
Asn	Ile	Glu	Glu	Lys	Gly	Glu	Lys	Asp	Phe	Val	Ser	Tyr	Val	Asp	Lys
		35					40					45			
Thr	Ser	Glu	Glu	Arg	Ile	Lys	Glu	Val	Ile	Leu	Lys	Phe	Phe	Pro	Asp
		50				55					60				
His	Glu	Val	Val	Gly	Glu	Met	Gly	Ala	Glu	Gly	Ser	Gly	Ser	Glu	
	65				70				75					80	
Tyr	Arg	Trp	Phe	Ile	Asp	Pro	Leu	Asp	Gly	Thr	Lys	Asn	Tyr	Ile	Asn
				85					90					95	
Gly	Phe	Pro	Ile	Phe	Ala	Val	Ser	Val	Gly	Leu	Val	Lys	Gly	Glu	Glu
		100					105						110		
Pro	Ile	Val	Gly	Ala	Val	Tyr	Leu	Pro	Tyr	Phe	Asp	Lys	Leu	Tyr	Trp
		115					120						125		

Gly	Ala	Lys	Gly	Leu	Gly	Ala	Tyr	Val	Asn	Gly	Lys	Arg	Ile	Lys	Val
130					135					140					
Lys	Asp	Asn	Glu	Ser	Leu	Lys	His	Ala	Gly	Val	Val	Tyr	Gly	Phe	Pro
145					150				155						160
Ser	Arg	Ser	Arg	Arg	Asp	Ile	Ser	Ile	Tyr	Leu	Asn	Ile	Phe	Lys	Asp
				165					170					175	
Val	Phe	Tyr	Glu	Val	Gly	Ser	Met	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Val
			180					185					190		
Asp	Leu	Cys	Met	Val	Ala	Glu	Gly	Ile	Phe	Asp	Gly	Met	Met	Glu	Phe
		195				200					205				
Glu	Met	Lys	Pro	Trp	Asp	Ile	Thr	Ala	Gly	Leu	Val	Ile	Leu	Lys	Glu
210					215						220				
Ala	Gly	Gly	Val	Tyr	Thr	Leu	Val	Gly	Glu	Pro	Phe	Gly	Val	Ser	Asp
225					230				235						240
Ile	Ile	Ala	Gly	Asn	Lys	Ala	Leu	His	Asp	Phe	Ile	Leu	Gln	Val	Ala
				245				250						255	
Lys	Lys	Tyr	Met	Glu	Val	Ala	Val								
			260												

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGCCCCGAGCG	TGTTGCCAAG	ATGCTTGAAA	GAATGCTATC	CAAGGCGGAA	TCTATGCTCG	60
GCGACGCCCCA	GAGGCTTATC	GAGGAGGGTA	AGGCCGTTGA	GGCTAAGAAG	CTGTTAGCGG	120
CTGCTCATAG	GCTAGTAGAT	CGCCTAGAGG	ATGCTCTCGA	CCACGCCCTC	AACCATATAG	180
AGCATCACAA	GGAACATCAT	GAGGAGCACC	ACAAGGAGCA	CGACTAACAA	CACTCTTAGA	240
ATCTCGAGAC	GAGCTTGCTT	CCCGTGTCTC	TCGCGCCTAG	CCAGTTTTTA	ATAGCCTAAG	300
CCGAGACCCA	CATTCCAACA	TTACTCCGTT	TGTCACTATC	ATGTTCTAAT	TGTCACACGC	360
CCCGTATAAA	TTGGGGGACC	TGGAGGAAGC	GTTGCCGGTG	ACCCCGCGTG	GCCAAGAAGG	420
CTGTCTGCCC	AATATGCGGT	GGCGATGTTG	AACTACCCGA	TAACGTAATG	GATGGCGAGA	480
TCGTGGAGCA	CGACTGTGGG	GCAATGCTAG	TCGTGAGGAT	CCGGGATGGC	AATGTTGTTC	540
TAGAGCAGTT	GGAGCGCGTT	GAGGAGGACT	GGGGAGAGTA	GAGGCTATGC	GCATAGCAAT	600
CGTTTTATGAC	CATCCGCGTG	TTGAGGAGAA	GAGGTTAGCT	GAGGAAGCGA	GGAAGCTTGG	660
TCACGAAACCT	TCCTCTTTTA	ATATTGACTC	GTTGCTCTTT	CGCCTTGATA	GCCTGGAGCG	720
CATTCTAGGC	GATGTTGATG	TAGTACTTCA	GAGGGCGGTG	AGTTACTTCA	AGGCTCTCGA	780
GTCTACAAGG	ATACTCGAGG	CTGCCGGCTA	CACTGTTCATC	AACAATAGTT	TAGTGCAGCT	840
TAACTGCGGC	GACAAACTAT	TGACAACGAT	CTTGCTTGCT	AAGCATGGTG	TGCCAACACC	900
GCGTGCATAC	GCTGCTTTTT	CGCGTGACAC	TGCTGTGCGG	GCTGCAGAGG	AGCTTGGATA	960
CCCCGTTGTT	GTCAAGCCCG	TCATTGGTAG	TTGGGGTAGG	CTTGTGGCTA	GGGCTGATTG	1020
CAGGGAGAGT	CTAGAGGCTG	TGATAGAGCA	TAGAGAGGTT	CTCGGCCCGG	CTTACTACAA	1080
GGTTCATTAT	GTGCAAGAGT	ATGTGCGCAA	GCCTCTACGT	GACATACGCG	TATTCGTGAT	1140
TGGTGATGAG	GTTCCCGTGG	CGATATACAG	GGTTAACGAG	CGTCATTGGA	AGACTAACAC	1200
GGCACTAGGC	GCCAAGGCCG	AGCCTGCGCC	AGTGACCCCC	GAGTTACGTG	AGTTAGCGCT	1260
TCGCGCGGCC	AAGGCTGTGG	GTGGCGGTGT	GCTTGGTATA	GATGTGTTTG	AAGACCCGGA	1320
GAGAGGCCCT	CTCGTGAACG	AGATTAAACG	GAAGCTCGAC	TTCAAGAACA	CTGAGAGGGT	1380
GACCGGGTTT	AACATGGCTA	GGGCTATCGT	CGAGTATGCA	GTGTCGGTCG	CGAAGAGGTG	1440
AATGGAATGG	ATAGGGTAGA	GGTGCTTCTG	GATGAGGCTA	GGCGTGGCGC	TATAGAGGGT	1500
GACGCTCGCC	GCGCATGTGA	AGCGGCATTA	AGGCTGGTTG	ACGTTGTGCT	CCGCGAGGGG	1560
CCTAGGGTTG	CACAGGAGTC	TGGGCGTGCG	ATTGAACCCG	GTGATGTACT	ACTAGCTGAG	1620
GCTCTGAGCT	TGAGAGCAGA	GCAGGTGAAG	GAGGAGCCCC	AGGCGGACAA	TTGTCTGGAG	1680
CTCGCAAAGG	CTGCATTCCG	CCTCTATAAG	CGGCTCCAGG	GGATGGAGTA	AAGTTCGCAG	1740
TGTGTTGCCC	GTTTTAGCCT	CTGCCTTACT	TTCTACTCGC	GTGAGGCGAG	TGTCCCTTGA	1800
CACGTTGCTG	GCGCGAGCTG	AGAAACGACC	TCGAGATGAT	ACCCGAGATC	GTCGAGAAGC	1860
AGATCGAGGA	GACGATAGTG	CCGGAGGGTC	TTGGCGAGCA	ACGACTTGTG	TTCATTGGCA	1920
GCGGTGATTC	TTTCGCGGCC	GCACTTGTAG	CCGAGCATGC	CGGCATAGGC	GTGCGACGCG	1980
ATCCTCTTGA	TGTGCTAGTG	GCTGGCGTTG	ATGGGCCTGG	CGACGCTATA	CTCCTAAGCG	2040

TTGGTGGGCG	CTCAAAACGA	GTTGTTGACG	CGGCTCGTTT	CCTGTCTTCA	CGTGGCTTTT	2100
GTATCATAGC	GGTCACGGGT	AACGAGAGGA	GTCCTCTCGC	ACGCACAGCA	CACGTTACCG	2160
TGAAGCTCGT	CTATTCTGAC	CTCGCCTGTG	GCATGGGCGC	CGCACGCCAT	GTCGCTATGC	2220
TTGCAGCGCT	CTCCGCATTG	TTCAACGCTA	GACCTCGTAT	ACCCGAGAAG	CTTGTTGAGG	2280
AGCCCCTGCC	TTTCGACCC	CAGGCTGTGT	ACGCGGGTGT	GGGCGTTGGT	GTAGCCTCTG	2340
CCCTGTTTCT	GGTGTGAAG	ATCTGCGAGT	TGCTCGCAGA	CTGCGCCACC	TGGTGGCATC	2400
TAGAGCAGTT	CGCACACGCA	CCTGTCTATG	GCACGAGAAG	CAATATACTC	GTCGTGTATC	2460
CGATCCTCGT	TGTGAGAGGA	GCACGCTAGA	GGAGTATCTC	TCGGCCTTCC	GGGAGGCCGG	2520
GTTTGAGGTC	ACCACTGTAC	CCGTGTTGAA	CGACCCTTGG	TCTACAGCTA	TTCTCCACGC	2580
TACGCTGGCC	ATCTCCAGTG	CTGCAGAGAC	CGCCTTCAGT	CGCGGCATTG	AGGAGCCGGG	2640
ATATCGTGCA	CATCCCGCGC	TTAGCAGGCT	AACCAGGCTG	ATCTACCTAG	AGGAGTAGAA	2700
CCTCTCGAGG	ACCGGTATGT	AGTGGTCTAG	AGGCTTCCCG	TCATGGTGTA	TCGCGAGGCC	2760
TATTCCTGCT	CTCCTCGCGC	CTTCCACGTT	GGGCTCATAA	TCATCTATGA	ATGCTGTTTT	2820
CGCTGGGTCC	GCGCGAAGGA	GTTGCATCGC	CGCCTCGTAT	ATCTTTGTGT	GTGGCTTGCA	2880
AAAGCCGACA	ATATCCCTCG	TAACCACCGT	ATCCACGAGG	TGGGCTAGAT	CGTCACGCTC	2940
TAGAAGTAGA	CGTACGCATT	CGTAGCACCA	GTTGTTTCGAG	ACTATGCCGA	CCAGTATCCC	3000
GTTTCTCTTG	GCCCATCTTA	GCAGCTCGTA	TGTACCCGGT	GCTACGTATA	CGCCAGACAG	3060
CACAGCTGAT	TGCAATACCC	TTGCTAATGC	CTCTGCCCTT	GAGGGGGTCG	GCGTCAAGCC	3120
GTGTTTTGCG	AGGAGCACGG	CAGCCGCATA	CACATATACT	TGTTGCACGG	AGCATCCAG	3180
CCTCCACGTG	TCCATTACAC	GCCTCACGCT	ATCCGGCGTC	GCGTCGGCCC	CTAGGGCACG	3240
TAGATGTCTG	GCAGCAGTCT	CGTAGAGAGT	CTCCTCGTAC	CACCTATTGT	TGAGGTAAAT	3300
GACGCCACCT	AAATCCAGCA	GGAGTGTAGG	GTTACGCGGC	AAGGCGCCTC	CTCATGTATT	3360
CGAGGAGGCC	GCCCCGTTGCC	AGAATTTTCA	CTACAACACC	CCGGAAGGGC	GGGAAACGGT	3420
ACGTCAACAC	CCTACCATCC	TTCTTGATGA	GCTTCGCTAC	ACCCTCGTCA	AGGTTTATCT	3480
CTATCTCGTC	GCCCTCCTCG	GCCGCCCTCCA	CGAGCTCTGG	GAGCACTATA	ACGGGGAGCC	3540
CGTTGTTAAT	CGCGTTACGG	TAGAATATTC	TCGAGAAGCT	CTTCGCTATG	ATGGCCTTGA	3600
CGCCTGCAGC	CTTGAGAGCT	ATCGCGGCTT	GCTCCCTGCT	ACTACCCATA	CCAAAGTTCC	3660
TACCCGCGAC	CAGCACTACA	CCCTTGAGCG	CCTTCTTGGG	GAACCTCCGA	TCCAGAGGCT	3720
CCATAGCATG	CTCGGCAAGC	TTCTCCGGCT	CAGTATATAC	CAGGTAGCGG	GCAGGGATAA	3780
TCACGTCCGT	GTTGATGTTA	TTGCCGTAAT	TGAGCACAGG	GCCCTTCACG	ACACCCAGGT	3840
TCAAGTAGAGG	TTTACCACAA	GTTTGCGCTC	GCTATCCCAG	GCTATAATCC	AGCTGTTTAC	3900
TCGGCCAGCT	TCACCCACAC	ACTTTTCAAC	TCCATTATCC	TTGTAGCGCA	ATCTACCCTT	3960
CTGGGTAGCA	CAGCGTTAAG	CCCATAGTGC	CAAGGCGCCA	CAATGATGCC	CTCCGGCACA	4020
TTCTCGTCGG	GTATCAGCCG	GAGGCGTATG	GCCCCCTCTT	CCGTCTCGAG	CCTAGCGTGA	4080
CCGGCGCCAG	CCTCCTTAGG	GTTGACTCGT	GCGTATAGCT	CGCCGCTCAC	ATCTAGCATC	4140
GCGTTTGTAT	AGTAGCTCAC	CGGGTCTCTT	GCAGTCACGA	GCACCTTCCT	ATCACCATCG	4200
GGCACGACCG	GCTCGACCGG	CGGGTATAGA	CGGACGCGTA	TCCTCGAGAC	ACGCCTGGGC	4260
AGGAGGTACT	CGCCTCTCTC	CGCAACCGCC	TTGGAGGAA			4299

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGGACTGATA	AAGAAAAAGA	AGAGGTTTAA	GGGCCTCAAT	ATTAAATTCT	ACACATTAGA	60
TATCCAAAAA	GGAGAATTAC	TTAATCTAGA	GACTTACCTT	AAGGAGTTAC	ATGAGTTCCT	120
TAGAGGCCTT	ACATTAAAAA	GAAAAGTAGA	AGAGGAACAA	TGACCCCGGA	AGAGCTCCTA	180
ACCCGCCTCG	AATTCAAAGG	AGTAACCCCTC	GAAAAGATGC	TCAATACTGC	GTTAGAGCTC	240
TACATCGGCG	ACGAGCGCGA	GAAAGTTTCA	GAAAGGCTGA	GAGAGCTGAT	GCTGAGGTAT	300
CTGGGCGACA	TCAACGTTCA	AGCTCTGCTC	TTTTTCGGCTC	TACTGCTCGA	AGAGAACTTC	360
AAGGTTGAGG	GCGACCCCGT	GAACCTTGTTG	GCCGACGAGC	TCATCGGCAT	GAACATCGCC	420
GAGCTCATAG	GTGGAAAGAT	GGCGCTCTTC	AACTTCTTCT	ACTACGACAC	CAAGAAGCCC	480
GGCATTTTAG	CCGAGCTTCC	GCCTTTCTCT	GACGATGCGA	TAGGGGGCTT	TATAGCGGGC	540
TGTATGACAA	GGCTGTTTCA	GGGGGTGTAC	GGTGCGGAAT	CTCTTACCCT	TCTTCACGCG	600
GATTCCGGTC	AAAGGCAACT	TCAAAAGGGT	TAGAAATGAG	CTCTGGGCAC	TTCCCATTCT	660
CGCACCCGTA	ACTTCGGCCC	TGGCGACGCT	CGTGGGCTCT	GTGCTCGCCG	GGGTAATAAT	720
CCTGGGCGGC	AACTACGCGT	TTCACCCAAC	GTCTCGGCAA	CCCACGTGCT	GATAACCCCTC	780
ATAGGCTTCG	TCGTGGTCTA	CAGCATACTG	TTCTACATCT	GGCTCCACTT	CGTCAGGAAG	840

CTCATCAGGG	AGGGCCCCGA	ACCGGTTGAG	GGTGACGTCA	CCGCGAAGCC	GACCCCTGCC	900
GTTAGCGCCG	CGGGAGGTGG	TCAGTGATGG	ACTACGCGAC	CGCATGGTTT	TACTTCTCCG	960
CCTTCCTCCT	CGGAATGTAC	TTAGCGTTTG	ATGGCTTCGA	CCTTGGCATA	GGCGCGTTGC	1020
TCGCCCTGAT	TAAGGACCAG	AGGGAGCGCG	ACATACTCGT	GAACACCATC	GCGCCGGTCT	1080
GGGACGGCAA	CGAGGTCTGG	TTCATCACCT	GGGGTGCCGG	GCTCTTCGCG	ATGTGGCCGG	1140
CGCTCTACGC	GACGCTCTTC	AGCACGTTCT	ACCTTGCCGT	CTGGCTGCTC	GCGTTCTGT	1200
TCATATTGAG	GGCTGTGCGC	TTTGAGTTCA	GGAACAAGAA	CAAGGAGCTA	TGGGACAAGC	1260
TCTTCGCTCT	CGTCAGCGCG	TTAATCCCGC	TCGTCATCGG	CGTCATAGTC	GGCAACCTCA	1320
TCATGGGAAT	TCCCATTGAC	GCCAAGGGCT	TCCACGGCTC	ACTGCTGACG	CTCTTCAGGC	1380
CCTACCCGCT	CATCGTCGGC	CTCTTCATAC	TCTTCGCGGT	GACCTGGCAC	GGAGCCAACT	1440
GGGGCGTCTA	CAAAACCACA	GGAAAGCTCC	AGGAGCAGAT	GAGGGAGCTC	GCCTTCAAGG	1500
CCTGGCTCCT	GACCGTCGTC	TTCTCTCTGC	TCACAGTCAT	CGGCATGAAA	ATCTGGGCCC	1560
CACTGAGGTT	CGAGAGGGCA	CTAACGCCGC	TTGGGCTCCT	CCTAACGGTT	GTCATCCTCG	1620
TGGCAGGACT	GCTCGACGGA	CAGCTCATCA	AGAAAGGGGA	GGAGAATTTG	GCCTTCTACA	1680
TCAGCTGGCT	GGCCTTCCCG	CTCGTTGTGT	TCCTCGTCTA	CTACACAATG	TACCCCTACT	1740
GGGTCATCTC	GACCACCGAT	CCGAACCTCA	AGCTCAGCAT	ACACGACCTC	GCGGCATCTC	1800
CGCTGACCTT	CAAGGCCGTC	TTGGGAATCT	CGCTGACCTT	GGCGGTCTATC	ATCATGGCCT	1860
ACACCTCTTA	CGTATACAGG	GCCTTCGGCG	GAAAGGTCAC	CGAGGCGGAG	GGCTACTACT	1920
GAGTTCCCTT	TTCTTTTTTC	GATATTGCAA	CTTTTTTAGG	GAAAAGTTTA	TAATTCGAGT	1980
CACCTAAGTT	CCTTCTGGAA	ACCTAAAAAA	CGGTGGTCGA	AATGCACAGA	GGCAGATCTA	2040
CCGGCTGGCC	CTACGACCGG	AAGCCGGTCC	TCGTCTTCTG	GGAAACCACC	AAAGCCTGCC	2100
GGCTCAAGTG	CAAGCACTGC	AGAGCGGAGG	CAATACTCCA	GGCACTGCCG	GGCGAGCTGA	2160
ACACGGAGTA	GGGAAAGGCC	CTCATCGATT	CCCTCACCGA	CTTCGGAAGG	CCCTACCCGA	2220
TACTCATTTCT	GACCCGTGGC	GACCCGCTCA	TGAGGAAGGA	CATCTTCGAG	CTCATCGAGT	2280
ACGCCGTTGA	GAAGGGCATT	CGCGTTGGTC	TCGCCCCCGC	TGTAACGCC	CTCCTGACCG	2340
AGGAAACAAT	CGAGAGAATC	GCGAGGAGCG	GAGTTAAGGC	GGTAAGCATA	AGCCTCGACA	2400
GCCCCGTTTCC	AGAAGTTCAC	GACGCAATCA	GAGGCATAGA	AGGGACGTGG	GAGAAAACCG	2460
TCTGGGCCAT	CAAGGAGTTC	CTGAAACACG	GCCTAAGCGT	TCAGGTGAAC	ACGGTTGTGA	2520
TGCGCGAGAC	CGTTGAAGGA	CTGCCCCAGA	TGGTGAAACT	GCTTAAAGAC	CTCGGCGTCG	2580
AAATCTGGGA	GGTCTTCTAC	CTCGTCCCCG	CCGGGAGGGG	CAACTTCGAG	AGCGACCTGA	2640
GGCCGGAGGA	GTGGGAGGAC	GTCACACACT	TCCTCTACGA	GGCCTCGAAG	CACCTCCTCG	2700
TGAGGACCAC	CGAGGGCCCCG	ATGTTTCAGGC	GAGTGGCGAT	AATGAGGAAA	GCCCTTGAGG	2760
AGAAGGGATT	CGACCCCGAC	GAGGTTCTCA	AGCCCCGGGA	GCTCTACTTC	CGGCTGAAGA	2820
AACGGCTCGT	TGAGCTTCTC	GGCGAGGGGA	ACGAGGCGAG	GGCCCAAAC	ATGGGAACGC	2880
GCGAGCGGAA	GGGAATAGTC	TTCATCGCCT	ACAACGGCAA	CGTCTACCCG	AGCGGTTTCC	2940
TGCCCTTCAG	CGTCGGCAAC	GTCCGCGAGA	AAAGTTTGGT	TGAGATTTAC	AGGGAGAGTG	3000
AACTTATGAA	AAAGCTCCGC	TCGGCCGAGT	TCGAGGGGCG	CTGCGGGAGG	TGCGAGTTCA	3060
GGGAAATCTG	CGGGGGAAGC	AGGGCGAGGG	CCTACGCCTA	TCGCTTAAAC	CCGCTCGCCG	3120
AAGACCCTGC	CTGCCCCGTAC	GAGCCGGGCT	CATACCTAAG	GCTCGCCAAA	AAGTTCAATC	3180
TTCACCTTCC	GATTGAGATT	TTTGGAGCCC	AAAAGCCGAT	TTGAGGTGAT	GGAAATGAGG	3240
TGGAAGGCTC	TTTTACTGAT	TGGAATCCTC	TCCTGTCTGT	TCCTCGGTGC	CGGATGCGTT	3300
GGCTCGAATA	CCTCAACTGA	AACCGGCCCA	TCCCAGAAGG	AAATAACCGT	GAAGGACTTC	3360
TCGGGAAGGA	ACATCACGGC	TAAAGTTCCG	GTTTCAGCGG	CGGTCTGTTCT	CTCGACTTCC	3420
GCCCTCGAAA	TAATCCAGCT	CCTCAACGCG	AGCGACCAGG	TCGTCCGTAT	TCCAAAGGAG	3480
GCCCAGTACG	ACGCTTTACT	GAGCGAAAGC	CTGAAGAACA	AGACCGTCGT	TGGCGCGAGG	3540
CTCAAGATTG	ACGACTGGGA	GAAGGTTTTA	GCCCTAAAGC	CCGACCTAAT	CATCGACCTC	3600
GACCTGAAGA	AGTTCTACAA	CGTTGACGAG	CTCCTCAACC	GCTCCGCCAG	CTACGGAATT	3660
CCGGTCTGTC	TGCTGAGGGA	GGATAACCTT	GAGGACATAC	CGAAGGCGGT	TTCTGCTCCTC	3720
GGTCAGCTCT	TCGGAAGGGA	GAAAGAGGCC	AAGGCCTTTC	ACGACTACTT	CAACGAGCAG	3780
GTGAAGGAGG	TTAAGGCCAT	AGCCTCAAAG	ATTCCAGCGG	AGGAGAGAAA	GAAGGCGATA	3840
ATGATACAGC	CGATAATGGG	CAAGCTCTAC	CTCGTCAACG	GCAACGACGT	CCTTGCTCAG	3900
GCCGTCAGGC	TCGTTGGGGC	GGACTACCTC	GTGAACCTGA	CCTTCAACGG	CTACACTCCG	3960
GTTAGGGTCC	CGATGGACGG	GGAGAAGATA	ATAGCGAACT	ACCGCGATGC	AGACGTCTGTA	4020
ATCCTCCTGA	CGAGCGCCGT	AACGCCTTAC	GACCAGGTCG	AGAAGCTCCG	GGAGGAGATG	4080
CTCAGCGACG	AGGCCTGGAG	GGGCATTAAG	GCCGTCAGGG	AGGGCAACGT	AGTAATCCTC	4140
AGGGCGGACA	TGGGTAAAGA	CTCCTTCCTC	CGCTGGAGCC	CGCGCTTGGC	AGTGGGAATC	4200
TGGGTCAATTG	GAAAGGCAAT	CTACCCGGAC	TACTATCCTG	ACTGGAACGA	CAAGGCCAAG	4260
GACTTTCTTA	AGAGGTTTTA	CGGCCTCTCC	TGATTTTTCT	TTTGGGGTGG	GACGATGATA	4320
CGGGTCTTTT	CAGCAGTCTT	CGCGGAAATC	GTCAAACCTC	TCGGGAAAGC	CGGGGAGATA	4380
GCCGGAGTGA	ACGAGGAAAT	CAGGTTTCGAC	CCCTGCCTGC	CGGAGCTGAA	GGATAAGCCT	4440
GTCATCGGAA	AGTACCTCAA	GCGGAGCAAG	AGGACCTACT	GGGACGTTTT	AGAGGAGCTT	4500
AGGCCGGACC	TTATCCTCGA	CTTCGATGTT	GAGAACCTGC	ACTCCGGGGA	CGAGCTGAGG	4560
GCCTTTGGGG	AGCGTATAGG	GGCAAGGGTC	GAGCTGATTG	ACTTCGAGAC	CGTTGAAGGC	4620
TTCGTCGAGG	CGAGCAGGAG	GATAGCCGAG	CTAACGAGGG	GCGACTTTTC	AAAGCTCGGC	4680
GGGTTCTATG	AGAAGCACCT	GACGAGGCTG	GGTGAGATAA	CTGAAGCCAT	CGAGGAGAGG	4740

CCTAAAGCCC	TGCTCACCTA	CCGGAAC TTC	AACGTCGTAA	CGAGGACCAA	CGTTCTGAGC	4800
GACGCGGTTA	GAAAAGCAGG	GGCGATGAAC	CTCGGCGAGA	GGATACGGAC	AAAGCGGAAG	4860
GTCTATCCGG	TAAAGAAGGA	GCGCTTCTTC	AGGTCTTCG	GCGATGCGGA	GCACCTCTTC	4920
CTGCTCACGA	GCATAATGAC	GGACAGGGAG	AAAATGGAGG	GGATAAGGGA	TGAAATCCTT	4980
GACTCGGCCG	AGTGGAGGGC	AATGGAAGCC	GTTCAGCTCG	GAAACGTGCA	CATAGTTGGC	5040
TCGGCCCTCG	ACCTTGAGAG	CTTCATGCGC	TGGAGTCCCC	GCATAATCCC	GGGAATCTAC	5100
CAGCTTGGAA	GGTTTATACA	CGGAACAAAT	CACCCACGAA	TCTCGTGGAA	ATCACTGCAA	5160
AAGTTTAAAA	TCCCCCTCCC	ACCCCTCGAA	GAACAAAAAC	GCATCGTTCG	CTACCTCGAC	5220
TCGATACACG	AGCGCGCCCA	AAAGCTGGTA	AAGCTCTACG	AGGAGCGGGA	GAAGGAGCTT	5280
GAGAAGCTTT	TCCCCGCGGT	GCTTGATAGG	GCGTTTAGGG	GTGAGCTGTG	ATTCCGGGAA	5340
TGGAATACGG	CTTTGAGAGG	GCAATCTTTG	AGATAGTCAG	CGGCTTTGTT	CTCTCCCTCG	5400
TAGTCAGGGC	TTTCGCTTAC	AGTTTGTGTC	TTCCATGGGT	ATCCTTTTTG	TTCAACGTTT	5460
TTTCGATACT	TCTGACAATA	GGCCTGATTG	ACAAAATGCC	CTTCTGGTCC	ATGTCATATC	5520

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGCTTGGATA	TCGAATTCCT	TATATGAAAA	ATTCATCGAA	TTGGTAAAAA	ACCACGATCT	60
TCATGTGGAA	ACTGGAATAT	TTGCTGCGCA	TATGCTTG TG	GAAATACATA	ACGATGGTCC	120
GGTGACTTTG	TTACTTGATT	CAAGAAAAGG	TATTTTGAAG	TCATCTTTGC	TGTCTCTAGG	180
AGGACTATAT	GCCTGAATAC	TCGCATAGCA	ATAAAAACAA	CTTTTTTGCC	GAAAACGATG	240
TGAAGAATTG	TCATCTACTG	CATGTATGTT	GTGCACCCGA	TTTGGCAATT	TCTTATTTGT	300
CCGGTGCACG	TGGTGATATT	TTCTTTTACA	ATCCTAACAT	ACATCCAAAA	GCTGAATACG	360
AGAAAACGACA	CGCCGAAGTG	ATTAAAAATTG	CTGCACCTCT	TAAAATGAAT	GTTCTGAAAG	420
TTCCCTTATAA	TCCTGACCTG	TTCTTCAAGC	TTACTAAAGG	ATTAAAAAAT	GAACCTGAAG	480
GCGGGACAAG	GTGCGAGATT	TGTATAAGAA	TGCGACTAGA	AAAAACAATG	GAATACGCGA	540
AAGAAAATGG	CTACAAAGAT	GTTTCCACAA	CGCTAACAGC	CTCTCCAAAG	AAAAATGTAG	600
CGATGATTGT	GAAGATAGGA	AAAGAACTGG	AAAAAAAATA	CGGTGTGGAA	TTTTTGCCTA	660
ATGTGTACCG	CAAAAGTCCG	CTTTACAACG	ATGCGCAAAA	GCTTATAACG	AAAATGGGTT	720
ATTTACAGAC	AAAAC TACTG	TGTTTGTATT	TTCTCAATAA	GAAC TCCGT	TATAGTAGCC	780
ACTCAAGAAA	CTAAAACCGT	AAAAAGTGGG	GTGCAAGTAT	GAAAATATAC	CACAAATTAG	840
AAGAAGTTGA	AGAACATAAG	CGGTCGTATG	CATCAATTGC	TTTTTTCATCG	AAAGTCAGGG	900
TTGAAATATGA	ACATGTGGC	AAAAAACTTG	CCCTCATCCC	TGTAAC TATT	GGAGACCTTA	960
CGGTGGTTAT	CGAAATTGAC	GATGATAGAG	AAGTATTCAA	TACTTTTGTTG	AACGAGCACA	1020
TCAAAAAC TC	TATCCTGAAA	CAGTTTCCGT	ATCCGGAAGA	GATTAGAGGG	TTAGCCAGAC	1080
ATTTTCGCAC	AGAATTGAAG	AATTT CAGAA	TCTTGGTTGT	AAAATACAAT	AGTGTCGAAG	1140
AAAAGGAATT	CTCAAGGTAT	TCACTGTCTA	ATATAACATT	CGGTGTGGTG	TCATACAATA	1200
AATTTGATGT	CCATT TTGTTA	CCAAGTAATG	TAAAAGTCAG	ACCGAAGCCA	GGATACTGTC	1260
TTTCACATGT	TGTCCAAAAG	CCTGAAGAAG	GTATCAGGCA	AGCATTC TTG	TTAGCCCGGT	1320
GGTTTGGTGG	TGGAAGCTAC	GACCAACTGC	CCAAATTAGC	GCTTGAAAGC	ACTGACATTG	1380
ACCTTGGA AA	GTGGACAAAT	ATAGTCAAAT	ACATCGTTCT	GTCAGATTTT	GAAAAGAGGT	1440
ATTTTTCTGG	TATAATAAAA	AAGCTAAACG	AATTTAGAAG	CGAGACATAT	TTTGACCCAT	1500
TTGCTAGGCT	TGAAATGATA	TCACTTGGCA	TAATACTCGC	CAAGTCAGAG	GGAGGAGGTA	1560
ACTTTGAACC	AGACAGTTAC	GATATCATTT	AGAGCACTTA	CTGAAAATAT	AAAATTAGCA	1620
CGAGTTGTTA	TACATACTTT	TCTAACATTC	CGAGGAGTGT	TCGATAAAGA	TATATT CGAT	1680
ACGGAATTGG	CTGTAAACGA	AGCGATTGCA	AACATTATTC	AGCATACATA	CAAAGGTGAA	1740
CCAAACTACG	TTGTGATGAC	GCTCAATTGG	ATAGAACCAG	ATACACTCGA	AGTGTTACTC	1800
CGCGATTTTG	GTCCAAAAGT	GGACCCAACG	AAAA TCAAAC	CACGAGATTT	AGATGATATC	1860
AGACCAGGAG	GACTCGGAGT	TTATATAATT	CAACGCATCT	TCGACATTAT	GGAATTTCCGA	1920
AACGTGAGTC	ATGGAAAATT	ACTTTATCTA	AAACGCTCCT	TCTTAATACC	TCCTAAAAAG	1980
CAGGAGCTTG	GGAATTTTAA	TAATGAACCC	TATCGAGAAT	ATTGAAAAAA	CCGTCAAAAC	2040
GGGGGAAAGA	AGACAAATGG	GCTTGCTCAC	AGGTTTGACA	AAAAATCCAT	CTTTCATGTC	2100
TGCATTTTTT	GGCTTTTTTG	CAGCACAATT	TTTGAAAGTG	GTGATATACA	AAGATTTCCG	2160
CGTATTTGGT	AGATACGGTG	GTATGCCCAG	TGCTCATGTT	GCAACAACCT	CAGCATTAGC	2220
TTGGGCTGTT	GGTTACACTA	CAGGTTTTGA	TTACCCGCTT	ACAGCCATCG	CTGCAATTTT	2280
CCTTGCTATT	ACAACAGCTG	ATGCTGTTGG	TTTACGAAGA	AATGTCGACC	CCAATAAAGG	2340

ACATACACTA	ATGGAAGCTA	TCTATGGCTT	CTTACTTGGG	TGGATAGTCG	CTCTGCTTAC	2400
GGTTAAGTTG	TATCGATAAT	TTTGAATGAG	TTGTAGTGAA	ATAGCCCAAG	TCTTTTTTTCG	2460
CAATTACATC	ATAATGCCAG	GAGGGTAATT	TACAATGTTT	TTTAGATTAC	CATTTTAAAGT	2520
TTTTGTTTTT	GCAGTTTTGT	TGCTTGCCAT	CTCGTTAACA	AGTGTGTGTA	GTTTTGGACA	2580
AGATGATGAG	CAGATAAAAA	CACCAAATTG	GTTTAGAAGT	GCGGTGATTA	AGAAAAGAGC	2640
TGGTATGAAT	CTAAAGACCG	CCCCAGAGTT	TGTAGATGAC	CTATGGAATG	CGATATACAC	2700
TATAGGCACA	AAATACAACG	TTCCCCAAC	GCTTATAGCC	GCTGTCAATT	CTGTAGAAAG	2760
CAACTTCGCC	AACGTGAAAG	GTGCTGGAGA	CGTGGTAGGA	ATGATGCAAA	TTTCTATCTC	2820
CACAGCCAAA	AATATATCGA	AACTCCTCGG	CCTCGAACAA	CCAAAAAACG	GTTGGGATGA	2880
GCTCCTCACA	AATTATTGGT	TGAATATAAC	TTACGGTACC	GCATACATCG	CTTATCTTTA	2940
CAAAAAGCAT	GGAACTTTAC	AGAAAGCGCT	CGAAGAATAC	AACAACGGAA	AAAATAAAAC	3000
TAAATACGCC	CAGCTGATAC	TACAACAATA	CAACCTATAC	GAGAGCCTCC	ATTCTGTGTA	3060
AATAAGAAAT	AACCAGCAAT	TGGATACAGA	TAATTCTTCG	ACATCTTCTG	AAGCAACAGA	3120
TACTTTGAAT	ACAACCAAGT	CAACAAATTC	ACAACCAACA	TCAGATGCAT	CAAATACATC	3180
AGTTAACACT	TCAGAAATCA	AGTTCCCGCC	TCTTTTCGGA	GTTGCAGGTT	ATTAAGATAT	3240
TTGTTCCGTA	GTTACTTAGG	AATGTGGGGT	GTATAGTTTG	GAAGATGAAA	AAATGAAACC	3300
TGAAACGATA	GTAAAAATTG	AACATTTATC	TTTTTCTTAC	CCGAGTTTCA	GTCTCAAAGA	3360
TGTAAGTTTT	GAGGTTTCGGA	AGGGAAGTTT	CTTCGGCATT	ATTGGACCAA	ATGGTTCGGG	3420
AAAAACCACG	CTACTCTCAC	TCATTATGAA	ATTCCAAAAG	CCAAAAAGTG	GGAAAATAAC	3480
AGTTGATGGG	AACGATGTGC	TCAGGCTATC	TCACAAAAAA	CTTGACAAAC	TTATAGCATA	3540
CATCGCTCAA	GACTTTAACC	CTACATACGA	TTTCACAGTT	GAAGAATTGG	TCGAAATGGG	3600
AGGAATCCCC	CGCTCACCAC	ATTTTTTTCGA	AACACCTGTT	TACGAGGAAG	AATTAGAAAA	3660
TGCACTCAAA	ACTGTTGATT	TGCTTGAATA	CCGAAAAAGA	ATATTCTCCA	CTCTTAGTGG	3720
AGGACAACAG	CGCAGGGTCT	TGATTGCACG	CGCAATCTAT	CAAAACACAC	CTATCATCAT	3780
TGCTGATGAA	TTGGTTAATC	ACTTGGATTT	AGGGCAAGCA	ATTAAAGTGT	TAGATTATCT	3840
AAAACAACCT	ACCGAATGTG	GAAAGACGAT	AATTGGACAT	TCCACCTGCA	GCCCCG	3896

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGTGCTGCA	AGGCGATTAA	GTTGGTAACG	CCAGGTTTTTC	CCAGTCACGA	CGTTGTAAAA	60
CGACGGCCAG	TGAATTGTAA	TACGACTCAC	TATAGGGCGA	ATTGGGTACC	GGGCCCCCCC	120
TCGAGGTCGA	CGGTATCGAT	AAGCTTGATA	TCGAATTCCG	TACGAAATGC	GGGAAAGAGA	180
GAAGGAAAAG	GAAAGAGAGC	ACAGATTTGG	AAATGAGACA	GAACACGAGG	AAGAGCATGG	240
TATGGCAGAG	CGTGAAAGAG	CACATGAGAA	CGAGTCTGAA	GAAATGGGCA	AGGGCGTTGG	300
CATGGGCGCC	CATGGAATGA	AGATGGGCAA	AGAAGCTCGC	GAAATGGTGA	AGGAAGAATA	360
CAAGGAAGCA	AAGGAGAGAT	ACAAGAAGGC	TAGAGAAGAG	TTTGAAAGAG	CAAAGAAGAT	420
GGGATTGGAC	ATCAGAGAGG	AGCGCGGATT	CAAGATGGCC	AAGGGATTCA	TGGTAGCTGG	480
ACTAGACGTT	GCTGAGATGT	GGCTGGAGAG	ACTGAAGGTA	CAGGTCATGA	ATATGGGTGA	540
AGAGGCCAAG	ATCACAGAGG	AGACCAAAT	GGAGCTGCTC	GCAAAGATCG	ACGAGAAGCT	600
TGCAGAAATC	AAAGAGCTGA	AGAACGAAAT	CAATGAGACC	TCCTCACCTG	AAGAGCTGAT	660
AGAAACTGTC	AAGAAAATCA	GAAAGGAGTG	GAGAGAAATC	AGAGATGAAA	TGAGGGCTCT	720
TACTGGCTAT	GTCCGCCGTT	CCAAGGTGGA	AAAGCTTGTT	GAAAAGGCCA	AGCAGGTAGA	780
GCTAATGCTT	GAGGCAAAGA	TCGAGGAGCT	CGATGCTGCA	GGAGTTGATA	CAACCAAAT	840
CGAGGCAACA	CTCGAGGACT	TCTCGGCAAA	GGTTAATGAA	GCAGAAGATT	TGATTGACAA	900
GGCTGAAAAT	CTGTTTCGAGG	AAGGCAACAT	TGCTGAAGGA	CACATGACTC	TCAAGGAAGC	960
CATAAAGACT	CTCAAGGAAG	CCTTCAAGGA	TGTCAAGGAA	GTTGTCAGCG	AGATGAAGGA	1020
AATGAACCAG	TATAGAGTTA	GGGAGGGCAA	GATCTTCTAC	GGAAACGAGA	CTGGAGAAGT	1080
CTGGGTGGAT	GGTAATGGTA	CTGCTGAGTT	TAACGGTACC	GGTATCGTTG	TGATCAGAGG	1140
AAACGCAACA	CTTGAGGTCG	CACCAAGAAG	TGCGATCGTG	ACACTGGTCG	GCTTCGGCGT	1200
GAAGAGCGTT	GAGGGTGGCG	TTTCAAGAGT	CAGCGGAGAA	GGTAAGGCAG	TAATCAGAGG	1260
AGAAAACCTC	ACCGTCAAGG	TGGAAGGTGA	CGACTTCAAG	CTCATAGTGA	AGGGCTACGG	1320
TACACTCAAA	CTCGATGGTG	AGGGTGAATA	CAGGGTAAAG	AAGAGCCAC	AGGAAGAGAT	1380
GACATTTAAA	CTCTTTCTTC	AACTCTAGCA	GTTTGAGCAT	TGCATTTCCA	AGATTTTTCG	1440
TGTTAGCTTC	GGGACAACCT	TGAAAATACG	TCGAGACAGG	CTCAAATGTT	GTCCCAGCAT	1500
TGCAGCTTTC	GGCAAAGCGA	ACGAGATTTG	CGTTCCGCTC	CCCAGCCCAA	CATGGCTTCT	1560

GTAATCTGAA	AAACTTTCAA	GTTCAACAGC	TTTCCCAAAA	ACATCCAAAA	GCTTTTCCGC	1620
AACACTTCTA	AATCTTTTCGA	GATTTATTGC	ATTTCTTTTC	ACCGAAATGC	TATCGGATTC	1680
TCTTCCCACA	ACCTCGATAT	GCGGCTCTTC	CAGAGCAATA	CCCACTCCAC	CGTCAATCCT	1740
TCCAACCTGG	CCGTTCAAAT	CAATGAGCGT	GATATGAATT	CTCGACGGAG	TTTTAACCTT	1800
AACATACATC	TATAGAATTT	AAACGGTAAT	TACTTAAGAA	GTTTTGGTTT	TGCGAAAAAG	1860
AGTTCAAAAT	TCATTCTTTT	AACTGCACTA	CAGCTCATCT	GTGCCTTTTC	TCCTTAATTC	1920
GATTTTTCTG	AGATAGTTCT	GGTATCTCGT	ATCAACTATG	TAAGCCTCGG	GAGCTATTAC	1980
AGGCAGATGA	TAACCGGTGA	ATATCCTTAT	TATCTCTCCA	GCCTGAACCG	AGCATGTCAG	2040
TGCATATGAT	ATCGGATCGT	GATCGATGTG	AGGATACTCC	ACCTCGAAGA	AAGACACACC	2100
ATCAGGCAGG	AAAGTAGTAA	TTATATCGGG	AATAAATGGA	GCTCCGAGCT	CTTCAGCAAC	2160
TTTTGTCAGC	ATTGAAATGT	GCTTATGAGC	AACAACAACA	TCAATACCTT	TCAACTGTCT	2220
CCTGAGTTCT	TTATAATCAT	GCGGGAAGGG	ATAAGAGATT	ATACACGAAT	CAGAACTCAT	2280
AGGATGCACA	ACATCATAAT	CGTTTGCTTC	AAGTGGCTTT	ATGCTGGCAT	CAAGCCTCAC	2340
ATCCATTGGT	GTAACATACAT	CTCCAATATA	CCGAATGCAA	CCAACACCAC	TTCTCCAGAG	2400
CAATTCCATG	AGCATTCTGC	TTCCGATGAC	AGCGACACTA	AAGTTCCTGA	GATAATCTAT	2460
CTTTTCTTCA	TCTGCCATCC	CATACCAGGA	AATTTTCTCT	ATGGCAATAG	CCCCGCATCC	2520
ATTAAATGGT	ATTAATTTTT	TGCCGTATTT	TGAGGAGGTA	GATATTAACC	AATTATTTTC	2580
AAACCATTTA	AGGGCATCGA	TGAAACATCC	CAAAACCAGT	TCAGCAAAAA	ATTAAATCAC	2640
TGCCACACAT	TGAGGACCCC	AAAATGGTGT	GAGAAATGGA	CGAACTGGGA	GGAGTTATTT	2700
TTGATCTGAT	AGAAGAGGAG	CCCGAAGTTG	AGGAGGACGA	CGAGATTAAG	CTCGCAGAGA	2760
TATACAGGCT	TGCTACAAAA	CTTATAAAGT	TACTCGAAGA	TCTCAAAAGC	CATGAGCTTA	2820
AAGAGTCAGC	ATCTCTTATG	CTCATAAAGG	AAATTATCGG	TGAAGACAGA	GTTCTGGTTG	2880
GTTTAGCATC	AAAAATGCTC	CAGGATATGA	GTCTCGGGTT	CGAAGAGGAC	GAAAAGTACG	2940
TTTCTTGATT	TTTGAACGTG	ATTTTCTACA	TGCTCTTTTC	CCAACCACAT	TCAGTTGCAT	3000
GCCATACGAA	AATTCCAATG	CCCAAATCCT	GGTAAATGTA	CTTTTTCATA	GTAAATGCTG	3060
CCAAACCCAG	ATTAAACTCA	ATTTTCATCAA	CAGGAAAAAG	AAAGAACGAA	AAAAAGACCT	3120
ACAACAGTCC	TATAATTGAC	CAAACCTTGAT	AGATTACAAA	CACCACAGTT	GGAATCAAAG	3180
CACAGATGAA	AGCTTTCCGG	ATTCCTGCAG	CC			3212

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATG GAA ATA ATA AAC AAA TTT CTA AAA AAA ATT GGA TAT AAG AAA GAT	48
Met Glu Ile Ile Asn Lys Phe Leu Lys Lys Ile Gly Tyr Lys Lys Asp	
1 5 10 15	
GGA GAA GAA AAA AAG GAC AAA TCT AAA ACC AAA ATA AAA ATT GAA GAA	96
Gly Glu Glu Lys Lys Asp Lys Ser Lys Thr Lys Ile Lys Ile Glu Glu	
20 25 30	
GAA AAA ACC ATG GAT ATC GAA ATT CCA AAA ATT GAA CCT ACT GAA AAT	144
Glu Lys Thr Met Asp Ile Glu Ile Pro Lys Ile Glu Pro Thr Glu Asn	
35 40 45	
TTT AAT CGT GAT GAA ATT GTT TTT GAG GAA GAT AAT GCC TAC GGT ATA	192
Phe Asn Arg Asp Glu Ile Val Phe Glu Glu Asp Asn Ala Tyr Gly Ile	
50 55 60	
TCC CAC AAA GGA AAT AGA ACA AAC AAC GAA GAC AAT ATT TTA ATT AGA	240
Ser His Lys Gly Asn Arg Thr Asn Asn Glu Asp Asn Ile Leu Ile Arg	
65 70 75 80	

AAA ATA AAA GAT ACC TAC ATA TTA GCA GTT GCA GAT GGT GTC GGA GGG	288
Lys Ile Lys Asp Thr Tyr Ile Leu Ala Val Ala Asp Gly Val Gly Gly	
85 90 95	
CAC AGC TCA GGA GAT GTT GCA TCA AAG ATG GCA GTG GAT ATT TTA GAA	336
His Ser Ser Gly Asp Val Ala Ser Lys Met Ala Val Asp Ile Leu Glu	
100 105 110	
AAC ATT ATC ATG GAA AAA TAC AAT GAA AAC CTA TCA ATT GAA GAG ATA	384
Asn Ile Ile Met Glu Lys Tyr Asn Glu Asn Leu Ser Ile Glu Glu Ile	
115 120 125	
AAA GAA CTT TTA AAA GAT GCA TAC ATT ACG GCA CAC AAC AAA ATA AAA	432
Lys Glu Leu Leu Lys Asp Ala Tyr Ile Thr Ala His Asn Lys Ile Lys	
130 135 140	
GAA AAC GCT ATT GGA GAT AAA GAG GGA ATG GGA ACA ACA CTA ACA ACT	480
Glu Asn Ala Ile Gly Asp Lys Glu Gly Met Gly Thr Thr Leu Thr Thr	
145 150 155 160	
GCA ATA GTT AAA GGG GAT AAA TGC GTT ATA GCA AAC TGC GGG GAT AGT	528
Ala Ile Val Lys Gly Asp Lys Cys Val Ile Ala Asn Cys Gly Asp Ser	
165 170 175	
AGG GCT TAT TTA ATT AGA GAT GGA GAA ATA GTT TTT AGA ACA AAA GAC	576
Arg Ala Tyr Leu Ile Arg Asp Gly Glu Ile Val Phe Arg Thr Lys Asp	
180 185 190	
CAC TCT TTG GTT CAG GTT TTA GTA GAT GAA GGA CAT ATT TCA GAG GAG	624
His Ser Leu Val Gln Val Leu Val Asp Glu Gly His Ile Ser Glu Glu	
195 200 205	
GAC GCA AGG CAT CAT CCA ATG AAA AAT ATC ATT ACC TCA GCA TTG GGA	672
Asp Ala Arg His His Pro Met Lys Asn Ile Ile Thr Ser Ala Leu Gly	
210 215 220	
TTG GAT GAA TTT AAG GTA GAT GAT TAC GAA TGG GAT TTA ATT GAT GGT	720
Leu Asp Glu Phe Lys Val Asp Asp Tyr Glu Trp Asp Leu Ile Asp Gly	
225 230 235 240	
GAT GTA TTA TTG ATG AGC TCC GAT GGG CTT CAT GAT TAT GTC AGT AAG	768
Asp Val Leu Leu Met Ser Ser Asp Gly Leu His Asp Tyr Val Ser Lys	
245 250 255	
GAA GAT ATT TTA AAA ACT GTA AAA AAT AAT GAT CAC CCA AAA GAT ATT	816
Glu Asp Ile Leu Lys Thr Val Lys Asn Asn Asp His Pro Lys Asp Ile	
260 265 270	
GTA GAT GAA TTA TTC AAT ACT GCA TTA AAA GAG ACA AGG GAC AAT GTG	864
Val Asp Glu Leu Phe Asn Thr Ala Leu Lys Glu Thr Arg Asp Asn Val	
275 280 285	
AGT ATT ATT CGT ATA	879
Ser Ile Ile Arg Ile	
290	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
Met Glu Ile Ile Asn Lys Phe Leu Lys Lys Ile Gly Tyr Lys Lys Asp
 1          5          10          15
Gly Glu Glu Lys Lys Asp Lys Ser Lys Thr Lys Ile Lys Ile Glu Glu
          20          25          30
Glu Lys Thr Met Asp Ile Glu Ile Pro Lys Ile Glu Pro Thr Glu Asn
          35          40          45
Phe Asn Arg Asp Glu Ile Val Phe Glu Glu Asp Asn Ala Tyr Gly Ile
          50          55          60
Ser His Lys Gly Asn Arg Thr Asn Asn Glu Asp Asn Ile Leu Ile Arg
          65          70          75          80
Lys Ile Lys Asp Thr Tyr Ile Leu Ala Val Ala Asp Gly Val Gly Gly
          85          90          95
His Ser Ser Gly Asp Val Ala Ser Lys Met Ala Val Asp Ile Leu Glu
          100          105          110
Asn Ile Ile Met Glu Lys Tyr Asn Glu Asn Leu Ser Ile Glu Glu Ile
          115          120          125
Lys Glu Leu Leu Lys Asp Ala Tyr Ile Thr Ala His Asn Lys Ile Lys
          130          135          140
Glu Asn Ala Ile Gly Asp Lys Glu Gly Met Gly Thr Thr Leu Thr Thr
          145          150          155          160
Ala Ile Val Lys Gly Asp Lys Cys Val Ile Ala Asn Cys Gly Asp Ser
          165          170          175
Arg Ala Tyr Leu Ile Arg Asp Gly Glu Ile Val Phe Arg Thr Lys Asp
          180          185          190
His Ser Leu Val Gln Val Leu Val Asp Glu Gly His Ile Ser Glu Glu
          195          200          205
Asp Ala Arg His His Pro Met Lys Asn Ile Ile Thr Ser Ala Leu Gly
          210          215          220
Leu Asp Glu Phe Lys Val Asp Asp Tyr Glu Trp Asp Leu Ile Asp Gly
          225          230          235          240
Asp Val Leu Leu Met Ser Ser Asp Gly Leu His Asp Tyr Val Ser Lys
          245          250          255
Glu Asp Ile Leu Lys Thr Val Lys Asn Asn Asp His Pro Lys Asp Ile
          260          265          270
Val Asp Glu Leu Phe Asn Thr Ala Leu Lys Glu Thr Arg Asp Asn Val
          275          280          285
Ser Ile Ile Arg Ile
          290
```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
ATG ACT CTG CTA GCC CTG TAT CAG AAT AAA CGT GTT ATC GTC AAG CTT      48
Met Thr Leu Leu Ala Leu Tyr Gln Asn Lys Arg Val Ile Val Lys Leu
 1          5          10          15

GGC TGG GGG AGC GGC ACT AGC CAA ATA ACT AAC GAG GCG CAA GTG CTG      96
Gly Trp Gly Ser Gly Thr Ser Gln Ile Thr Asn Glu Ala Gln Val Leu
```

20						25						30						
AGC Ser	GTA Val	TTG Leu 35	CAC His	GAT Asp	ATG Met	CCT Pro	ATA Ile 40	GTG Val	CCC Pro	AGA Arg	CTG Leu	CAT His 45	ACC Thr	CGT Arg	CTA Leu	144		
GAC Asp	TTA Leu 50	GAT Asp	GAT Asp	GTC Val	AAG Lys	CTC Leu 55	GTT Val	GCG Ala	ATA Ile	GAG Glu	TAC Tyr 60	ATA Ile	CCC Pro	TAC Tyr	AAG Lys	192		
AGC Ser 65	CTT Leu	AAC Asn	GCC Ala	GTC Val	GGC Gly 70	CGC Arg	TTG Leu	AAC Asn	CCC Pro	CTT Leu 75	AAG Lys	GCT Ala	GTC Val	ACA Thr	GCC Ala 80	240		
GTC Val	TTC Phe	TAT Tyr	ACA Thr	CTC Leu 85	GCA Ala	TCG Ser	CTA Leu	GTC Val	CAT His 90	ATC Ile	CAC His	GGC Gly	CGT Arg	GGT Gly 95	TTT Phe	288		
GCT Ala	CAT His	TGC Cys	GAC Asp 100	CTA Leu	AAG Lys	CCG Pro	GGT Gly	AAC Asn 105	GTT Val	ATA Ile	CCA Pro	GTT Val 110	CCC Pro	AAG Lys	CGT Arg	336		
GGC Gly	ATG Met	GTG Val 115	TTC Phe	ATC Ile	GAC Asp	TTT Phe	GGT Gly 120	GTT Val	GCA Ala	CGA Arg	CCT Pro	TTT Phe 125	GAC Asp	GCT Ala	GCG Ala	384		
GGC Gly 130	TTC Phe	GCG Ala	GCA Ala	GGA Gly	ACA Thr	CCA Pro 135	GGG Gly	TAT Tyr	ACG Thr	TGC Cys	CCA Pro 140	GAG Glu	GCT Ala	CTC Leu	GGC Gly	432		
GGC Gly 145	GAG Glu	ACC Thr	CCC Pro	GGC Gly	TCT Ser 150	GGC Gly	TGC Cys	GAT Asp	CTC Leu	TAC Tyr 155	AGC Ser	CTT Leu	GCC Ala	GGC Gly	ATA Ile 160	480		
TAC Tyr	TAC Tyr	TAC Tyr	TTG Leu	GTT Val 165	ACC Thr	GGG Gly	TTA Leu	AGC Ser	CCG Pro 170	CCA Pro	CGC Arg	GAC Asp	CCA Pro	AAA Lys 175	GAG Glu	528		
TTC Phe	GCC Ala	AAG Lys	GCG Ala 180	CTC Leu	TCG Ser	TTG Leu	GCT Ala	CCC Pro 185	GCT Ala	CCA Pro	AGT Ser	AGC Ser	CTC Leu 190	TTG Leu	GAA Glu	576		
CTG Leu	TTC Phe	ACA Thr 195	CAG Gln	CTG Leu	GTG Val	CTG Leu	GAT Asp 200	CCC Pro	GAG Glu	TAT Tyr	CGT Arg	AAC Asn 205	AGC Ser	CTT Leu	GAT Asp	624		
CCT Pro	CTC Leu 210	CAG Gln	CTG Leu	TTG Leu	AAG Lys	ATT Ile 215	GTT Val	GCA Ala	TCT Ser	TTT Phe	AAC Asn 220	CCG Pro	CAA Gln	CTG Leu	CTA Leu	672		
GTC Val 225	CCT Pro	CAT His	ATC Ile	GTT Val	ATA Ile 230	GAT Asp	GGT Gly	GTT Val	TAC Tyr	AAG Lys 235	CCG Pro	CTA Leu	GGT Gly	TAC Tyr	GGC Gly 240	720		
GAG Glu	GTA Val	AGC Ser	ATA Ile	GGC Gly 245	TCT Ser	AGA Arg	GGC Gly	GTT Val	ATA Ile 250	CGT Arg	GTT Val	GAT Asp	GGA Gly	CGA Arg 255	CCA Pro	768		
GTG Val	TAC Tyr	CTC Leu	GCG Ala 260	GTT Val	AAG Lys	AGG Arg	CAT His	GTG Val 265	AGG Arg	GGC Gly	ACA Thr	AGT Ser	ATG Met 270	TAC Tyr	GCG Ala	816		
TAT Tyr	ACG Thr	GAT Asp 275	CTT Leu	GTC Val	GTG Val	TTT Phe 280	AGG Arg	AGA Arg	GGC Gly	GAG Glu	AAA Lys 285	CTC Leu	ATA Ile	GTG Val	AGA Arg	864		

AGC	GGT	GAG	AGT	ATA	GAC	CTA	GAG	TTT	AAC	GAC	CTG	GTG	TTG	TTC	GAC	912
Ser	Gly	Glu	Ser	Ile	Asp	Leu	Glu	Phe	Asn	Asp	Leu	Val	Leu	Phe	Asp	
290						295					300					
AAC	CAC	ATA	CTA	TAC	GTA	TTT	ATC	CTT	CCG	GAA	AGG	CCC				951
Asn	His	Ile	Leu	Tyr	Val	Phe	Ile	Leu	Pro	Glu	Arg	Pro				
305					310					315						

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Thr	Leu	Leu	Ala	Leu	Tyr	Gln	Asn	Lys	Arg	Val	Ile	Val	Lys	Leu	
1				5					10					15		
Gly	Trp	Gly	Ser	Gly	Thr	Ser	Gln	Ile	Thr	Asn	Glu	Ala	Gln	Val	Leu	
			20				25						30			
Ser	Val	Leu	His	Asp	Met	Pro	Ile	Val	Pro	Arg	Leu	His	Thr	Arg	Leu	
		35					40					45				
Asp	Leu	Asp	Asp	Val	Lys	Leu	Val	Ala	Ile	Glu	Tyr	Ile	Pro	Tyr	Lys	
	50					55				60						
Ser	Leu	Asn	Ala	Val	Gly	Arg	Leu	Asn	Pro	Leu	Lys	Ala	Val	Thr	Ala	
	65				70				75						80	
Val	Phe	Tyr	Thr	Leu	Ala	Ser	Leu	Val	His	Ile	His	Gly	Arg	Gly	Phe	
				85					90					95		
Ala	His	Cys	Asp	Leu	Lys	Pro	Gly	Asn	Val	Ile	Pro	Val	Pro	Lys	Arg	
			100					105					110			
Gly	Met	Val	Phe	Ile	Asp	Phe	Gly	Val	Ala	Arg	Pro	Phe	Asp	Ala	Ala	
	115						120					125				
Gly	Phe	Ala	Ala	Gly	Thr	Pro	Gly	Tyr	Thr	Cys	Pro	Glu	Ala	Leu	Gly	
	130					135					140					
Gly	Glu	Thr	Pro	Gly	Ser	Gly	Cys	Asp	Leu	Tyr	Ser	Leu	Ala	Gly	Ile	
	145				150					155					160	
Tyr	Tyr	Tyr	Leu	Val	Thr	Gly	Leu	Ser	Pro	Pro	Arg	Asp	Pro	Lys	Glu	
			165						170					175		
Phe	Ala	Lys	Ala	Leu	Ser	Leu	Ala	Pro	Ala	Pro	Ser	Ser	Leu	Leu	Glu	
			180					185					190			
Leu	Phe	Thr	Gln	Leu	Val	Leu	Asp	Pro	Glu	Tyr	Arg	Asn	Ser	Leu	Asp	
		195					200					205				
Pro	Leu	Gln	Leu	Leu	Lys	Ile	Val	Ala	Ser	Phe	Asn	Pro	Gln	Leu	Leu	
	210					215					220					
Val	Pro	His	Ile	Val	Ile	Asp	Gly	Val	Tyr	Lys	Pro	Leu	Gly	Tyr	Gly	
	225					230				235					240	
Glu	Val	Ser	Ile	Gly	Ser	Arg	Gly	Val	Ile	Arg	Val	Asp	Gly	Arg	Pro	
				245					250					255		
Val	Tyr	Leu	Ala	Val	Lys	Arg	His	Val	Arg	Gly	Thr	Ser	Met	Tyr	Ala	
			260					265					270			
Tyr	Thr	Asp	Leu	Val	Val	Phe	Arg	Arg	Gly	Glu	Lys	Leu	Ile	Val	Arg	
		275					280					285				
Ser	Gly	Glu	Ser	Ile	Asp	Leu	Glu	Phe	Asn	Asp	Leu	Val	Leu	Phe	Asp	
	290					295					300					
Asn	His	Ile	Leu	Tyr	Val	Phe	Ile	Leu	Pro	Glu	Arg	Pro				
305					310					315						

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATG GAC ATC AGG GCC GTT GTT TTT GAC CTC GAC GGG ACG CTT GTG GGT	48
Met Asp Ile Arg Ala Val Val Phe Asp Leu Asp Gly Thr Leu Val Gly	
1 5 10 15	
GCT GAG AAG ACT TTC AGC GAG ATA AAG TCC GAG CTT AAA GAA CGG CTG	96
Ala Glu Lys Thr Phe Ser Glu Ile Lys Ser Glu Leu Lys Glu Arg Leu	
20 25 30	
ATT TCC TTA GGG ATT CCC AGG GAG CTC GTT GGA GAG CTA ACG CCG ATG	144
Ile Ser Leu Gly Ile Pro Arg Glu Leu Val Gly Glu Leu Thr Pro Met	
35 40 45	
TAT GAG GGC CTT ATC GAG CTG TCC AGA AAA ACG GGC AGA CCT TTC GAA	192
Tyr Glu Gly Leu Ile Glu Leu Ser Arg Lys Thr Gly Arg Pro Phe Glu	
50 55 60	
GAG ATG TAC TCA ATT CTC GTC AAT CTT GAA GTT GAA AGG ATA AGG GAC	240
Glu Met Tyr Ser Ile Leu Val Asn Leu Glu Val Glu Arg Ile Arg Asp	
65 70 75 80	
AGC TTT CTC TTC GAG GGG GCA AGG GAG CTC CTC GAC TTT CTT GTG GGG	288
Ser Phe Leu Phe Glu Gly Ala Arg Glu Leu Leu Asp Phe Leu Val Gly	
85 90 95	
GAG GGA ATA AAG CTT GCC CTC ATG ACC CGG AGC TCC AGA ATG GCT GCC	336
Glu Gly Ile Lys Leu Ala Leu Met Thr Arg Ser Ser Arg Met Ala Ala	
100 105 110	
CTT GAG GCC CTG GAG CTT CAC GGC ATT AAG GAC TAC TTT GAG ATT ATT	384
Leu Glu Ala Leu Glu Leu His Gly Ile Lys Asp Tyr Phe Glu Ile Ile	
115 120 125	
TCA ACG AGG GAT GAT GTC CCT CCC GAG GAG CTG AAA CCG AAT CCT GGC	432
Ser Thr Arg Asp Asp Val Pro Pro Glu Glu Leu Lys Pro Asn Pro Gly	
130 135 140	
CAG CTG AGG AGA ATC CTC GGT GAG CTC AAC GTT CAA CCA GAG AAA GCC	480
Gln Leu Arg Arg Ile Leu Gly Glu Leu Asn Val Gln Pro Glu Lys Ala	
145 150 155 160	
ATC GTC GTT GGA GAC CAC GGC TAC GAT GTC ATC CCT GCC CGG GAG CTC	528
Ile Val Val Gly Asp His Gly Tyr Asp Val Ile Pro Ala Arg Glu Leu	
165 170 175	
GGC GCT CTG AGC GTC CTT GTC ACC GGC CAC GAG GCT GGC AGA ATG AGC	576
Gly Ala Leu Ser Val Leu Val Thr Gly His Glu Ala Gly Arg Met Ser	
180 185 190	
TTT CAG GTT GAA GCC GAG CCA AAC TTT GAG GTC GAG AAC CTC ATT CAC	624
Phe Gln Val Glu Ala Glu Pro Asn Phe Glu Val Glu Asn Leu Ile His	
195 200 205	

CTC AGG AAG CTC TTC GAG AGG CTC CTG TCG AGC TAC GTT GTT GTT CCC Leu Arg Lys Leu Phe Glu Arg Leu Leu Ser Ser Tyr Val Val Val Pro 210 215 220	672
GCT TAC AAC GAG GAG AAG ACC ATC AAG GGG GTA ATA GAG AAT CTT CTC Ala Tyr Asn Glu Glu Lys Thr Ile Lys Gly Val Ile Glu Asn Leu Leu 225 230 235 240	720
AGG TAT TTC AAA AAG GAC GAG ATA ATC GTC GTG AAC GAC GGC TCC AGG Arg Tyr Phe Lys Lys Asp Glu Ile Ile Val Val Asn Asp Gly Ser Arg 245 250 255	768
GAT AGA ACG GAG GAG ATA GCT CGT TCT TAC GGA GTC CAC GTT CTT ACG Asp Arg Thr Glu Glu Ile Ala Arg Ser Tyr Gly Val His Val Leu Thr 260 265 270	816
CAT CTC GTC AAC AGG GGG CTT GGT GGG GCC CTC GGA ACG GGC TTT GCC His Leu Val Asn Arg Gly Leu Gly Gly Ala Leu Gly Thr Gly Phe Ala 275 280 285	864
TAT GCC ATC AGA AAA AAC GCC AAA CTT GTC CTC ACA TTT GAT GCC GAC Tyr Ala Ile Arg Lys Asn Ala Lys Leu Val Leu Thr Phe Asp Ala Asp 290 295 300	912
GGC CAG CAC CTT ATA AGC GAC GCC CTC CGC GTC ATG AGG CCA GTT GCG Gly Gln His Leu Ile Ser Asp Ala Leu Arg Val Met Arg Pro Val Ala 305 310 315 320	960
GAG GGC AGG GCG GAC TTT GCG GTC GGC TCA AGG CTC AAA GGT GAC ACG Glu Gly Arg Ala Asp Phe Ala Val Gly Ser Arg Leu Lys Gly Asp Thr 325 330 335	1008
AGC CAG ATG CCC CTC GTG AAG AAG TTC GGC AAC TTC GTT CTA GAT GCC Ser Gln Met Pro Leu Val Lys Lys Phe Gly Asn Phe Val Leu Asp Ala 340 345 350	1056
GTG ACC GCG GTT TTT GCT GGT AAA TAC GTC AGC GAC AGT CAG AGC GGG Val Thr Ala Val Phe Ala Gly Lys Tyr Val Ser Asp Ser Gln Ser Gly 355 360 365	1104
TTA AGG TGT CTA AGC GGC GAC TGC CTG AGG AAA ATC AGG ATA ACC TGC Leu Arg Cys Leu Ser Gly Asp Cys Leu Arg Lys Ile Arg Ile Thr Cys 370 375 380	1152
GAC CGC TAT GCC GTG TCG AGT GAG ATT ATA ATA GAG GCC TCC AAA GCG Asp Arg Tyr Ala Val Ser Ser Glu Ile Ile Ile Glu Ala Ser Lys Ala 385 390 395 400	1200
GGC TGT AGA ATT GTC GAA GTT CCT ATC AAG GCT GTT TAC ACT GAG TAC Gly Cys Arg Ile Val Glu Val Pro Ile Lys Ala Val Tyr Thr Glu Tyr 405 410 415	1248
TTT ATG AAG AAG GGG ACG AAC GTT TTA GAG GGC GTT AAG ATA GCC CTG Phe Met Lys Lys Gly Thr Asn Val Leu Glu Gly Val Lys Ile Ala Leu 420 425 430	1296
AAC CTT CTC TTT GAC AAA CTG AGG Asn Leu Leu Phe Asp Lys Leu Arg 435 440	1320

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 440 amino acids

(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

Met 1	Asp	Ile	Arg	Ala 5	Val	Val	Phe	Asp	Leu 10	Asp	Gly	Thr	Leu	Val 15	Gly
Ala	Glu	Lys	Thr	Phe	Ser	Glu	Ile	Lys	Ser	Glu	Leu	Lys	Glu	Arg	Leu
			20					25					30		
Ile	Ser	Leu	Gly	Ile	Pro	Arg	Glu	Leu	Val	Gly	Glu	Leu	Thr	Pro	Met
		35					40					45			
Tyr	Glu	Gly	Leu	Ile	Glu	Leu	Ser	Arg	Lys	Thr	Gly	Arg	Pro	Phe	Glu
	50				55					60					
Glu	Met	Tyr	Ser	Ile	Leu	Val	Asn	Leu	Glu	Val	Glu	Arg	Ile	Arg	Asp
	65			70					75					80	
Ser	Phe	Leu	Phe	Glu	Gly	Ala	Arg	Glu	Leu	Asp	Phe	Leu	Val	Gly	
			85					90					95		
Glu	Gly	Ile	Lys	Leu	Ala	Leu	Met	Thr	Arg	Ser	Ser	Arg	Met	Ala	Ala
			100					105					110		
Leu	Glu	Ala	Leu	Glu	Leu	His	Gly	Ile	Lys	Asp	Tyr	Phe	Glu	Ile	Ile
		115					120					125			
Ser	Thr	Arg	Asp	Asp	Val	Pro	Pro	Glu	Glu	Leu	Lys	Pro	Asn	Pro	Gly
	130				135					140					
Gln	Leu	Arg	Arg	Ile	Leu	Gly	Glu	Leu	Asn	Val	Gln	Pro	Glu	Lys	Ala
145				150				155						160	
Ile	Val	Val	Gly	Asp	His	Gly	Tyr	Asp	Val	Ile	Pro	Ala	Arg	Glu	Leu
			165					170					175		
Gly	Ala	Leu	Ser	Val	Leu	Val	Thr	Gly	His	Glu	Ala	Gly	Arg	Met	Ser
			180					185					190		
Phe	Gln	Val	Glu	Ala	Glu	Pro	Asn	Phe	Glu	Val	Glu	Asn	Leu	Ile	His
		195					200					205			
Leu	Arg	Lys	Leu	Phe	Glu	Arg	Leu	Leu	Ser	Ser	Tyr	Val	Val	Val	Pro
	210				215						220				
Ala	Tyr	Asn	Glu	Glu	Lys	Thr	Ile	Lys	Gly	Val	Ile	Glu	Asn	Leu	Leu
225				230					235					240	
Arg	Tyr	Phe	Lys	Lys	Asp	Glu	Ile	Ile	Val	Val	Asn	Asp	Gly	Ser	Arg
			245					250					255		
Asp	Arg	Thr	Glu	Glu	Ile	Ala	Arg	Ser	Tyr	Gly	Val	His	Val	Leu	Thr
			260					265					270		
His	Leu	Val	Asn	Arg	Gly	Leu	Gly	Gly	Ala	Leu	Gly	Thr	Gly	Phe	Ala
		275					280					285			
Tyr	Ala	Ile	Arg	Lys	Asn	Ala	Lys	Leu	Val	Leu	Thr	Phe	Asp	Ala	Asp
	290				295						300				
Gly	Gln	His	Leu	Ile	Ser	Asp	Ala	Leu	Arg	Val	Met	Arg	Pro	Val	Ala
305				310					315					320	
Glu	Gly	Arg	Ala	Asp	Phe	Ala	Val	Gly	Ser	Arg	Leu	Lys	Gly	Asp	Thr
			325					330					335		
Ser	Gln	Met	Pro	Leu	Val	Lys	Lys	Phe	Gly	Asn	Phe	Val	Leu	Asp	Ala
			340					345					350		
Val	Thr	Ala	Val	Phe	Ala	Gly	Lys	Tyr	Val	Ser	Asp	Ser	Gln	Ser	Gly

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATG GAA AAT CTT GAA AAA CTC CTT GAA GTG GCA AAG ATG GCA GCC CTT	48
Met Glu Asn Leu Glu Lys Leu Leu Glu Val Ala Lys Met Ala Ala Leu	
1 5 10 15	
GCC GGA GGA CAG GTA TTA AAG GAA AAC TTC GGA AAG ATT AAG CTT GAA	96
Ala Gly Gly Gln Val Leu Lys Glu Asn Phe Gly Lys Ile Lys Leu Glu	
20 25 30	
AAC ATT GAA GAA AAG GGA GAG AAG GAC TTC GTG AGC TAC GTT GAT AAA	144
Asn Ile Glu Glu Lys Gly Glu Lys Asp Phe Val Ser Tyr Val Asp Lys	
35 40 45	
ACC TCC GAA GAG AGA ATA AAA GAG CTA ATA CTT AAG TTC TTT CCC GAC	192
Thr Ser Glu Glu Arg Ile Lys Glu Leu Ile Leu Lys Phe Phe Pro Asp	
50 55 60	
CAC GAG GTC GTG GGG GAG GAA AGG GGA AAG GAG GGA AAA GAA AGC CCT	240
His Glu Val Val Gly Glu Glu Arg Gly Lys Glu Gly Lys Glu Ser Pro	
65 70 75 80	
TAC AAA TGG TTC ATA GAC CCC CTT GAT GGG ACC AAG AAC TAC ATA AAG	288
Tyr Lys Trp Phe Ile Asp Pro Leu Asp Gly Thr Lys Asn Tyr Ile Lys	
85 90 95	
GGC TTT CCC ATA TTT GCA GTC TCC GTC GGA CTC GTT AAG GAA AAC GAA	336
Gly Phe Pro Ile Phe Ala Val Ser Val Gly Leu Val Lys Glu Asn Glu	
100 105 110	
CCT ATA GTG GGA GCG GTT TAC CTT CCT TAC TTT GAT ACC CTA TAC TGG	384
Pro Ile Val Gly Ala Val Tyr Leu Pro Tyr Phe Asp Thr Leu Tyr Trp	
115 120 125	
GCT TCA AAG GGA AGG GGA GCC TAT AAA AAC GGG GAG AGG ATA AGC GTA	432
Ala Ser Lys Gly Arg Gly Ala Tyr Lys Asn Gly Glu Arg Ile Ser Val	
130 135 140	
AAG GAA AGG GGG GAG CTC AAG CAC GCG GCG GTT GTT TAC GGA TTT CCA	480
Lys Glu Arg Gly Glu Leu Lys His Ala Ala Val Val Tyr Gly Phe Pro	
145 150 155 160	
TCA AGA AGC AGG AGG GAT ATA TCT CTT TAC CTG AAT GTG TTT AAA GAG	528
Ser Arg Ser Arg Arg Asp Ile Ser Leu Tyr Leu Asn Val Phe Lys Glu	
165 170 175	
GTC TTT TAC GAA GTA GGT TCC GTT AGG AGG CCC GGG GCC GCA GCG GTT	576
Val Phe Tyr Glu Val Gly Ser Val Arg Arg Pro Gly Ala Ala Ala Val	
180 185 190	

GAT	ATA	TGC	ATG	CTT	GCG	GAG	GGC	ATA	TTT	GAC	GGG	ATG	ATG	GAG	TTT	624
Asp	Ile	Cys	Met	Leu	Ala	Glu	Gly	Ile	Phe	Asp	Gly	Met	Met	Glu	Phe	
	195						200					205				
GAG	ATG	AAG	CCA	TGG	GAC	ATA	ACG	GCG	GGA	CTC	GTA	ATA	CTG	AAG	GAA	672
Glu	Met	Lys	Pro	Trp	Asp	Ile	Thr	Ala	Gly	Leu	Val	Ile	Leu	Lys	Glu	
	210						215				220					
GCT	GGA	GGA	TTT	TAC	ACA	CTG	AAG	GGA	GAC	CCC	TTC	GGC	ATC	TCG	GAC	720
Ala	Gly	Gly	Phe	Tyr	Thr	Leu	Lys	Gly	Asp	Pro	Phe	Gly	Ile	Ser	Asp	
	225					230				235					240	
ATA	ATA	GCG	GGA	AAC	AGG	ATG	CTC	CAC	GAC	TTC	ATT	CTC	AAG	GTT	GTG	768
Ile	Ile	Ala	Gly	Asn	Arg	Met	Leu	His	Asp	Phe	Ile	Leu	Lys	Val	Val	
				245					250					255		
AAT	AAA	TAC	ATG	AAT	AAT	GAA	AGC	ACG								795
Asn	Lys	Tyr	Met	Asn	Asn	Glu	Ser	Thr								
			260					265								

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Glu	Asn	Leu	Glu	Lys	Leu	Leu	Glu	Val	Ala	Lys	Met	Ala	Ala	Leu	
1				5				10					15			
Ala	Gly	Gly	Gln	Val	Leu	Lys	Glu	Asn	Phe	Gly	Lys	Ile	Lys	Leu	Glu	
			20					25					30			
Asn	Ile	Glu	Glu	Lys	Gly	Glu	Lys	Asp	Phe	Val	Ser	Tyr	Val	Asp	Lys	
		35					40					45				
Thr	Ser	Glu	Glu	Arg	Ile	Lys	Glu	Leu	Ile	Leu	Lys	Phe	Phe	Pro	Asp	
	50					55					60					
His	Glu	Val	Val	Gly	Glu	Glu	Arg	Gly	Lys	Glu	Gly	Lys	Glu	Ser	Pro	
	65				70					75				80		
Tyr	Lys	Trp	Phe	Ile	Asp	Pro	Leu	Asp	Gly	Thr	Lys	Asn	Tyr	Ile	Lys	
			85					90					95			
Gly	Phe	Pro	Ile	Phe	Ala	Val	Ser	Val	Gly	Leu	Val	Lys	Glu	Asn	Glu	
			100					105					110			
Pro	Ile	Val	Gly	Ala	Val	Tyr	Leu	Pro	Tyr	Phe	Asp	Thr	Leu	Tyr	Trp	
		115					120					125				
Ala	Ser	Lys	Gly	Arg	Gly	Ala	Tyr	Lys	Asn	Gly	Glu	Arg	Ile	Ser	Val	
	130					135				140						
Lys	Glu	Arg	Gly	Glu	Leu	Lys	His	Ala	Ala	Val	Val	Tyr	Gly	Phe	Pro	
	145				150					155				160		
Ser	Arg	Ser	Arg	Arg	Asp	Ile	Ser	Leu	Tyr	Leu	Asn	Val	Phe	Lys	Glu	
			165					170					175			
Val	Phe	Tyr	Glu	Val	Gly	Ser	Val	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Val	
		180					185					190				
Asp	Ile	Cys	Met	Leu	Ala	Glu	Gly	Ile	Phe	Asp	Gly	Met	Met	Glu	Phe	
		195					200					205				
Glu	Met	Lys	Pro	Trp	Asp	Ile	Thr	Ala	Gly	Leu	Val	Ile	Leu	Lys	Glu	
	210					215					220					
Ala	Gly	Gly	Phe	Tyr	Thr	Leu	Lys	Gly	Asp	Pro	Phe	Gly	Ile	Ser	Asp	
	225				230					235					240	
Ile	Ile	Ala	Gly	Asn	Arg	Met	Leu	His	Asp	Phe	Ile	Leu	Lys	Val	Val	
				245					250					255		

Asn Lys Tyr Met Asn Asn Glu Ser Thr  
260 265

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATG AGT GAA CAG CCG GTA TTG TCT GTT CAA GGA TTA AGC GGC GGG TAT	48
Met Ser Glu Gln Pro Val Leu Ser Val Gln Gly Leu Ser Gly Tyr	
1 5 10 15	
AGC ATG AAC CGA CCG GTT CTG CAT GAC GTA ACC TTT CAG GTT GAA CCG	96
Ser Met Asn Arg Pro Val Leu His Asp Val Thr Phe Gln Val Glu Pro	
20 25 30	
GGT GAG ATG GTG GGT TTG ATC GGC CTG AAC GGT GCG GGC AAG AGT ACC	144
Gly Glu Met Val Gly Leu Ile Gly Leu Asn Gly Ala Gly Lys Ser Thr	
35 40 45	
ACG ATG AAG CAT ATT CTC GGG CTG ATG AAT CCG CAA AAA GGC AGC ATT	192
Thr Met Lys His Ile Leu Gly Leu Met Asn Pro Gln Lys Gly Ser Ile	
50 55 60	
CAG GTT CAA GGA AAG AGC CGG ACA GAG CAT TCG GAA GCC TAT CAC GGC	240
Gln Val Gln Gly Lys Ser Arg Thr Glu His Ser Glu Ala Tyr His Gly	
65 70 75 80	
GCC TTG GCG TTT GTT CCC GAA TCC CCG CTG CTG TAT GAG GAG ATG ACA	288
Ala Leu Ala Phe Val Pro Glu Ser Pro Leu Leu Tyr Glu Glu Met Thr	
85 90 95	
GTA CGA GAG CAT CTG GAA TTT ACG GCG CGC TCC TAT GGC GTA TCC CGT	336
Val Arg Glu His Leu Glu Phe Thr Ala Arg Ser Tyr Gly Val Ser Arg	
100 105 110	
GAA GAT TAT GAG GCA CGT TCG GAG CAG CTG TCG AAG ATG TTC CGT ATG	384
Glu Asp Tyr Glu Ala Arg Ser Glu Gln Leu Ser Lys Met Phe Arg Met	
115 120 125	
GAA GAG AAG ATG GAC AGC CTG TCC ACG CAT TTG TCC AAA GGC ATG CGC	432
Glu Glu Lys Met Asp Ser Leu Ser Thr His Leu Ser Lys Gly Met Arg	
130 135 140	
CAA AAA GTG ATG ATC ATG TGC GCA TTC GTA GCC AGA CCG TCC CTG TAC	480
Gln Lys Val Met Ile Met Cys Ala Phe Val Ala Arg Pro Ser Leu Tyr	
145 150 155 160	
ATC ATT GAC GAG CCC TTT CTT GGG CTT GAT CCG CTT GGC ATA CGC TCG	528
Ile Ile Asp Glu Pro Phe Leu Gly Leu Asp Pro Leu Gly Ile Arg Ser	
165 170 175	
CTG CTT GAC TTC ATG CTG GAG CTG AAG GCA TCC GGC GCT TCG GTA TTG	576
Leu Leu Asp Phe Met Leu Glu Leu Lys Ala Ser Gly Ala Ser Val Leu	

180

185

190

CTA AGC TCC CAC ATT  
 Leu Ser Ser His Ile  
 195

591

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Ser	Glu	Gln	Pro	Val	Leu	Ser	Val	Gln	Gly	Leu	Ser	Gly	Gly	Tyr
1				5					10					15	
Ser	Met	Asn	Arg	Pro	Val	Leu	His	Asp	Val	Thr	Phe	Gln	Val	Glu	Pro
		20						25					30		
Gly	Glu	Met	Val	Gly	Leu	Ile	Gly	Leu	Asn	Gly	Ala	Gly	Lys	Ser	Thr
		35					40					45			
Thr	Met	Lys	His	Ile	Leu	Gly	Leu	Met	Asn	Pro	Gln	Lys	Gly	Ser	Ile
	50					55				60					
Gln	Val	Gln	Gly	Lys	Ser	Arg	Thr	Glu	His	Ser	Glu	Ala	Tyr	His	Gly
	65				70				75					80	
Ala	Leu	Ala	Phe	Val	Pro	Glu	Ser	Pro	Leu	Leu	Tyr	Glu	Glu	Met	Thr
			85					90						95	
Val	Arg	Glu	His	Leu	Glu	Phe	Thr	Ala	Arg	Ser	Tyr	Gly	Val	Ser	Arg
			100					105					110		
Glu	Asp	Tyr	Glu	Ala	Arg	Ser	Glu	Gln	Leu	Ser	Lys	Met	Phe	Arg	Met
		115					120					125			
Glu	Glu	Lys	Met	Asp	Ser	Leu	Ser	Thr	His	Leu	Ser	Lys	Gly	Met	Arg
	130					135					140				
Gln	Lys	Val	Met	Ile	Met	Cys	Ala	Phe	Val	Ala	Arg	Pro	Ser	Leu	Tyr
	145				150					155				160	
Ile	Ile	Asp	Glu	Pro	Phe	Leu	Gly	Leu	Asp	Pro	Leu	Gly	Ile	Arg	Ser
			165					170					175		
Leu	Leu	Asp	Phe	Met	Leu	Glu	Leu	Lys	Ala	Ser	Gly	Ala	Ser	Val	Leu
			180					185					190		
Leu	Ser	Ser	His	Ile											
			195												

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...1482

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATG	AAG	AAA	ATA	ACT	ATT	AGT	AGT	TTG	CTT	CTA	CTT	TTA	CTT	ATT	TCT
Met	Lys	Lys	Ile	Thr	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Ile	Ser
1				5				10						15	

48

ACC AAT TTG AAT CTC GCA TAC GAT TCC CAA GAG AGC GGT ATT AAA AAT	96
Thr Asn Leu Asn Leu Ala Tyr Asp Ser Gln Glu Ser Gly Ile Lys Asn	
20 25 30	
ATA ATA ATC CTC ATT GGA GAC GGC ATG GGA ATG AGT CAT GTC CAG ATT	144
Ile Ile Ile Leu Ile Gly Asp Gly Met Gly Met Ser His Val Gln Ile	
35 40 45	
ACA AAG CTT GTT TAT GGT CAT CTA AAC ATG GAA GAG TTC CCA ATT ATT	192
Thr Lys Leu Val Tyr Gly His Leu Asn Met Glu Glu Phe Pro Ile Ile	
50 55 60	
GGA TTC GAA CTT ACT GAG TCA TTA AGT GGG GAA GTT ACG GAC TCC GCT	240
Gly Phe Glu Leu Thr Glu Ser Leu Ser Gly Glu Val Thr Asp Ser Ala	
65 70 75 80	
GCA GCA GGA ACT GCA ATA GCA ACT GGA GTC AAA ACA TAT AAT CGA ATG	288
Ala Ala Gly Thr Ala Ile Ala Thr Gly Val Lys Thr Tyr Asn Arg Met	
85 90 95	
ATT TCA GTT ACT AAC ATA ACT GGA AAA GTT ACA AAT CTA ACT ACC TTG	336
Ile Ser Val Thr Asn Ile Thr Gly Lys Val Thr Asn Leu Thr Thr Leu	
100 105 110	
CTT GAA ATA GCC CAG GTA CTT GGA AAA TCA ACT GGA CTT GTG ACT ACT	384
Leu Glu Ile Ala Gln Val Leu Gly Lys Ser Thr Gly Leu Val Thr Thr	
115 120 125	
ACT AGA ATT ACA CAC GCA ACC CCT GCA GTA TTT GCT TCC CAC GTT CCT	432
Thr Arg Ile Thr His Ala Thr Pro Ala Val Phe Ala Ser His Val Pro	
130 135 140	
GAC AGA GAT ATG GAA GAG GAA ATA GCG AGA CAG CTC ATA GCT CAC CGG	480
Asp Arg Asp Met Glu Glu Glu Ile Ala Arg Gln Leu Ile Ala His Arg	
145 150 155 160	
GTC AAC GTC CTA TTA GGT GGA GGG AGA AAG AAA TTT GAC GAG AAT ACC	528
Val Asn Val Leu Leu Gly Gly Gly Arg Lys Lys Phe Asp Glu Asn Thr	
165 170 175	
CTA AAA ATG GCA AAA GAA CAG GGA TAT AAT ATA GTC TTC ACG AAA GAA	576
Leu Lys Met Ala Lys Glu Gln Gly Tyr Asn Ile Val Phe Thr Lys Glu	
180 185 190	
GAG CTC GAG AAA GCA GAG GGT GAG TTT ATT CTA GGG CTT TTT GCA GAT	624
Glu Leu Glu Lys Ala Glu Gly Glu Phe Ile Leu Gly Leu Phe Ala Asp	
195 200 205	
AGC CAC ATT CCT TAC GTA TTG GAC AGA AAA CCA GAA GAT GTT GGA CTT	672
Ser His Ile Pro Tyr Val Leu Asp Arg Lys Pro Glu Asp Val Gly Leu	
210 215 220	
TTG GAA ATG ACT AAA AAA GCA ATT TCA ATA CTA GAG AAA AAT CCA AAT	720
Leu Glu Met Thr Lys Lys Ala Ile Ser Ile Leu Glu Lys Asn Pro Asn	
225 230 235 240	
GGG TTC TTT CTC ATG ATT GAA GGG GGC AGA ATT GAT CAT GCA GCT CAT	768
Gly Phe Phe Leu Met Ile Glu Gly Gly Arg Ile Asp His Ala Ala His	
245 250 255	
GAG AAT GAT ATA GCA TCA GTT GTT GCA GAG ACT AAG GAG TTT GAT GAC	816
Glu Asn Asp Ile Ala Ser Val Val Ala Glu Thr Lys Glu Phe Asp Asp	
260 265 270	

GTT GTT GGA TAT GTT CTT GAG TAT GCA AAA AAG AGG GGA GAT ACA CTA Val Val Gly Tyr Val Leu Glu Tyr Ala Lys Lys Arg Gly Asp Thr Leu 275 280 285	864
GTA ATA GTG CTG GCT GAC CAT GAG ACA GGG GGG CTT GGA TTA GGT CTA Val Ile Val Leu Ala Asp His Glu Thr Gly Gly Leu Gly Leu Gly Leu 290 295 300	912
ACA TAT GGA GAT GCA ATT AAT GAA GAT GTC ATC AGG AAC ATA AAC GCT Thr Tyr Gly Asp Ala Ile Asn Glu Asp Val Ile Arg Asn Ile Asn Ala 305 310 315 320	960
AGT GTG TCG AAA ATT GCT AGT GAA ATA AGG GCA ACG AAT GAC ATA AAG Ser Val Ser Lys Ile Ala Ser Glu Ile Arg Ala Thr Asn Asp Ile Lys 325 330 335	1008
AGA GTT ATC AAA AAA TAT ACT GGA TTC GAG CTA ACA GAG GAC GAA ATT Arg Val Ile Lys Lys Tyr Thr Gly Phe Glu Leu Thr Glu Asp Glu Ile 340 345 350	1056
AAT TAC ATT GAG GAA GCT ATA AAC TTA GCA GAC GAA TAT GCG CTT CAA Asn Tyr Ile Glu Glu Ala Ile Asn Leu Ala Asp Glu Tyr Ala Leu Gln 355 360 365	1104
AAT GCA ATA GCT GAT ATT ATA AAC AAA CGC GTT GGT GTA GGT TTT GTA Asn Ala Ile Ala Asp Ile Ile Asn Lys Arg Val Gly Val Gly Phe Val 370 375 380	1152
TCC CAC AAA CAT ACA GGA GCT CCT GTT TCA CTT CTA GCC TAC GGC CCA Ser His Lys His Thr Gly Ala Pro Val Ser Leu Leu Ala Tyr Gly Pro 385 390 395 400	1200
GGT GCA GAG AAT TTT GCA GGC TTT TTA CAC CAT GTA GAT ACG GCA AAG Gly Ala Glu Asn Phe Ala Gly Phe Leu His His Val Asp Thr Ala Lys 405 410 415	1248
CTA ATT GCC AAG CTA ATG CTC TTT GGG AAG AAA GAT ATT CCC GTT ACC Leu Ile Ala Lys Leu Met Leu Phe Gly Lys Lys Asp Ile Pro Val Thr 420 425 430	1296
ATC TTG GGA ATA AGT GGA GTT AAA GGA GAT ATA ACC GGA GAC TTC AAA Ile Leu Gly Ile Ser Gly Val Lys Gly Asp Ile Thr Gly Asp Phe Lys 435 440 445	1344
GTG GAT GAG CAA GAT GCA TAT GTG ACC TTA ATG ATG TTG CTT GGG GAA Val Asp Glu Gln Asp Ala Tyr Val Thr Leu Met Met Leu Leu Gly Glu 450 455 460	1392
AGG GTA GAT ACT GAA CTT GAA AGG AAA GTC GAC ATG AAT AAT AAC GGC Arg Val Asp Thr Glu Leu Glu Arg Lys Val Asp Met Asn Asn Asn Gly 465 470 475 480	1440
ATA ATC GAG TTG GGA GAC GTG CTC CTG ATT CTA CAA GAG TCC Ile Ile Glu Leu Gly Asp Val Leu Leu Ile Leu Gln Glu Ser 485 490	1482

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met	Lys	Lys	Ile	Thr	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Leu	Ile	Ser
1				5				10					15	
Thr	Asn	Leu	Asn	Leu	Ala	Tyr	Asp	Ser	Gln	Glu	Ser	Gly	Ile	Asn
			20				25					30		
Ile	Ile	Ile	Leu	Ile	Gly	Asp	Gly	Met	Gly	Met	Ser	His	Val	Gln
		35				40				45				Ile
Thr	Lys	Leu	Val	Tyr	Gly	His	Leu	Asn	Met	Glu	Glu	Phe	Pro	Ile
	50					55				60				Ile
Gly	Phe	Glu	Leu	Thr	Glu	Ser	Leu	Ser	Gly	Glu	Val	Thr	Asp	Ser
65					70					75				80
Ala	Ala	Gly	Thr	Ala	Ile	Ala	Thr	Gly	Val	Lys	Thr	Tyr	Asn	Arg
				85					90					95
Ile	Ser	Val	Thr	Asn	Ile	Thr	Gly	Lys	Val	Thr	Asn	Leu	Thr	Leu
			100					105				110		
Leu	Glu	Ile	Ala	Gln	Val	Leu	Gly	Lys	Ser	Thr	Gly	Leu	Val	Thr
	115						120					125		
Thr	Arg	Ile	Thr	His	Ala	Thr	Pro	Ala	Val	Phe	Ala	Ser	His	Val
	130				135					140				Pro
Asp	Arg	Asp	Met	Glu	Glu	Ile	Ala	Arg	Gln	Leu	Ile	Ala	His	Arg
145					150				155					160
Val	Asn	Val	Leu	Leu	Gly	Gly	Gly	Arg	Lys	Lys	Phe	Asp	Glu	Asn
			165					170					175	Thr
Leu	Lys	Met	Ala	Lys	Glu	Gln	Gly	Tyr	Asn	Ile	Val	Phe	Thr	Lys
		180					185					190		Glu
Glu	Leu	Glu	Lys	Ala	Glu	Gly	Glu	Phe	Ile	Leu	Gly	Leu	Phe	Ala
	195						200					205		Asp
Ser	His	Ile	Pro	Tyr	Val	Leu	Asp	Arg	Lys	Pro	Glu	Asp	Val	Gly
	210					215					220			Leu
Leu	Glu	Met	Thr	Lys	Lys	Ala	Ile	Ser	Ile	Leu	Glu	Lys	Asn	Pro
225					230					235				Asn
Gly	Phe	Phe	Leu	Met	Ile	Glu	Gly	Gly	Arg	Ile	Asp	His	Ala	Ala
			245						250				255	His
Glu	Asn	Asp	Ile	Ala	Ser	Val	Val	Ala	Glu	Thr	Lys	Glu	Phe	Asp
		260						265					270	Asp
Val	Val	Gly	Tyr	Val	Leu	Glu	Tyr	Ala	Lys	Lys	Arg	Gly	Asp	Thr
	275						280					285		Leu
Val	Ile	Val	Leu	Ala	Asp	His	Glu	Thr	Gly	Gly	Leu	Gly	Leu	Gly
	290					295					300			
Thr	Tyr	Gly	Asp	Ala	Ile	Asn	Glu	Asp	Val	Ile	Arg	Asn	Ile	Asn
305					310					315				Ala
Ser	Val	Ser	Lys	Ile	Ala	Ser	Glu	Ile	Arg	Ala	Thr	Asn	Asp	Ile
			325						330				335	Lys
Arg	Val	Ile	Lys	Lys	Tyr	Thr	Gly	Phe	Glu	Leu	Thr	Glu	Asp	Glu
		340						345				350		Ile
Asn	Tyr	Ile	Glu	Glu	Ala	Ile	Asn	Leu	Ala	Asp	Glu	Tyr	Ala	Leu
	355						360					365		Gln
Asn	Ala	Ile	Ala	Asp	Ile	Ile	Asn	Lys	Arg	Val	Gly	Val	Gly	Phe
	370					375					380			Val
Ser	His	Lys	His	Thr	Gly	Ala	Pro	Val	Ser	Leu	Ala	Tyr	Gly	Pro
385					390					395				400
Gly	Ala	Glu	Asn	Phe	Ala	Gly	Phe	Leu	His	His	Val	Asp	Thr	Ala
			405					410					415	Lys
Leu	Ile	Ala	Lys	Leu	Met	Leu	Phe	Gly	Lys	Lys	Asp	Ile	Pro	Val
		420						425					430	Thr
Ile	Leu	Gly	Ile	Ser	Gly	Val	Lys	Gly	Asp	Ile	Thr	Gly	Asp	Phe
	435						440					445		Lys
Val	Asp	Glu	Gln	Asp	Ala	Tyr	Val	Thr	Leu	Met	Met	Leu	Leu	Gly
	450					455					460			Glu
Arg	Val	Asp	Thr	Glu	Leu	Glu	Arg	Lys	Val	Asp	Met	Asn	Asn	Asn
465					470					475				Gly
Ile	Ile	Glu	Leu	Gly	Asp	Val	Leu	Leu	Ile	Leu	Gln	Glu	Ser	

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...954

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATG	ATT	AAC	CAA	ATA	AAC	TTC	AAA	ACC	TCT	CAT	GGA	GGA	AGC	AGA	GAA	48
Met	Ile	Asn	Gln	Ile	Asn	Phe	Lys	Thr	Ser	His	Gly	Gly	Ser	Arg	Glu	
1				5					10					15		
GAA	GGC	TAC	ATA	AAC	TTC	TCG	GCC	TCT	GTA	AAT	CCT	TAT	CCA	CCA	GAA	96
Glu	Gly	Tyr	Ile	Asn	Phe	Ser	Ala	Ser	Val	Asn	Pro	Tyr	Pro	Pro	Glu	
			20					25					30			
TGG	ACT	GAT	GAA	ATG	TTT	GAG	AGG	GCT	AAA	AAG	ATA	AGC	ACC	TTC	TAT	144
Trp	Thr	Asp	Glu	Met	Phe	Glu	Arg	Ala	Lys	Lys	Ile	Ser	Thr	Phe	Tyr	
		35					40					45				
CCT	TAC	TAT	GAA	AAG	CTT	GAG	GAA	GAA	CTC	TCA	GAT	CTA	ATT	GGG	GAG	192
Pro	Tyr	Tyr	Glu	Lys	Leu	Glu	Glu	Glu	Leu	Ser	Asp	Leu	Ile	Gly	Glu	
		50				55					60					
CCA	ATA	ACT	ATA	ACT	GCA	GGA	ATA	ACA	GAG	GCA	CTT	TAC	CTG	CTT	GGA	240
Pro	Ile	Thr	Ile	Thr	Ala	Gly	Ile	Thr	Glu	Ala	Leu	Tyr	Leu	Leu	Gly	
65					70				75						80	
GTT	TGG	ATG	AGG	GGT	CGG	AAA	GTA	ATA	ATC	CCG	AAG	CAC	ACC	TAT	GGG	288
Val	Trp	Met	Arg	Gly	Arg	Lys	Val	Ile	Ile	Pro	Lys	His	Thr	Tyr	Gly	
				85					90					95		
GAA	TAC	GAG	AGG	ATC	TCA	CGC	ATG	TTC	GGA	GGT	AGG	GTG	ATC	AAA	GGT	336
Glu	Tyr	Glu	Arg	Ile	Ser	Arg	Met	Phe	Gly	Gly	Arg	Val	Ile	Lys	Gly	
			100					105					110			
CCC	AAT	GAC	CCA	GGA	AAG	TTA	GCA	GAA	TTT	GTT	GAA	AGA	AAT	TCA	TTC	384
Pro	Asn	Asp	Pro	Gly	Lys	Leu	Ala	Glu	Phe	Val	Glu	Arg	Asn	Ser	Phe	
		115					120					125				
GTG	TTC	TTC	TGC	AAT	CCA	AAC	AAT	CCA	GAT	GGA	AAG	TTC	TAC	CGA	GAA	432
Val	Phe	Phe	Cys	Asn	Pro	Asn	Asn	Pro	Asp	Gly	Lys	Phe	Tyr	Arg	Glu	
	130					135					140					
AAA	GAG	ATG	AAA	CCT	CTT	TTA	GAT	GCC	ATT	CAA	GAC	ACT	AAC	TCA	ATT	480
Lys	Glu	Met	Lys	Pro	Leu	Leu	Asp	Ala	Ile	Gln	Asp	Thr	Asn	Ser	Ile	
145					150				155						160	
TTG	ATC	TTG	GAT	GAA	GCC	TTC	ATA	GAC	TTT	GTT	AAG	AAA	CCA	GAA	AGC	528
Leu	Ile	Leu	Asp	Glu	Ala	Phe	Ile	Asp	Phe	Val	Lys	Lys	Pro	Glu	Ser	
			165						170					175		
CCA	GAG	GGA	GAG	AAC	ATA	ATC	AGG	CTA	AGG	ACT	TTT	ACC	AAA	AGC	TAC	576
Pro	Glu	Gly	Glu	Asn	Ile	Ile	Arg	Leu	Arg	Thr	Phe	Thr	Lys	Ser	Tyr	
			180					185					190			

GGG CTC CCA GGG GTA AGG GTT GGA TAT GTT ATT GGA TTT GTC GAT GCT	624
Gly Leu Pro Gly Val Arg Val Gly Tyr Val Ile Gly Phe Val Asp Ala	
195 200 205	
TTC AGG AGC GTT AGA ATG CCA TGG TCA ATT GGC TCT ACT GGG GTG GCC	672
Phe Arg Ser Val Arg Met Pro Trp Ser Ile Gly Ser Thr Gly Val Ala	
210 215 220	
TTC TTA GAG TTC TTA CTC AAA GAT AAC TTC AAA CAC TTA AGA AAA ACC	720
Phe Leu Glu Phe Leu Leu Lys Asp Asn Phe Lys His Leu Arg Lys Thr	
225 230 235 240	
CTC CCC CTA ATA TGG AAA GAA AAG GAG AGG ATT GAG AAA GAA TTG AAA	768
Leu Pro Leu Ile Trp Lys Glu Lys Glu Arg Ile Glu Lys Glu Leu Lys	
245 250 255	
GTT AAA AGC GAT GCA AAT TTC TTC ATT ATG AAG GTC AGA GAA GGA ATA	816
Val Lys Ser Asp Ala Asn Phe Phe Ile Met Lys Val Arg Glu Gly Ile	
260 265 270	
ATT GAA AAG CTA AAA GAG AAT GGC ATC CTT GTA AGG GAT TGC AAG AGC	864
Ile Glu Lys Leu Lys Glu Asn Gly Ile Leu Val Arg Asp Cys Lys Ser	
275 280 285	
TTT GGA CTC CCT GGG TAC ATA AGG TTT TCA GTT AGA AGG AGA GAA GAG	912
Phe Gly Leu Pro Gly Tyr Ile Arg Phe Ser Val Arg Arg Arg Glu Glu	
290 295 300	
AAT GAC AAA CTC ATA AAC ATC CTT AGA AAA ACA CTT AAT ACT	954
Asn Asp Lys Leu Ile Asn Ile Leu Arg Lys Thr Leu Asn Thr	
305 310 315	

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ile	Asn	Gln	Ile	Asn	Phe	Lys	Thr	Ser	His	Gly	Gly	Ser	Arg	Glu
1				5					10					15	
Glu	Gly	Tyr	Ile	Asn	Phe	Ser	Ala	Ser	Val	Asn	Pro	Tyr	Pro	Pro	Glu
			20					25					30		
Trp	Thr	Asp	Glu	Met	Phe	Glu	Arg	Ala	Lys	Lys	Ile	Ser	Thr	Phe	Tyr
		35					40					45			
Pro	Tyr	Tyr	Glu	Lys	Leu	Glu	Glu	Glu	Leu	Ser	Asp	Leu	Ile	Gly	Glu
		50				55					60				
Pro	Ile	Thr	Ile	Thr	Ala	Gly	Ile	Thr	Glu	Ala	Leu	Tyr	Leu	Leu	Gly
		65			70				75					80	
Val	Trp	Met	Arg	Gly	Arg	Lys	Val	Ile	Ile	Pro	Lys	His	Thr	Tyr	Gly
			85					90						95	
Glu	Tyr	Glu	Arg	Ile	Ser	Arg	Met	Phe	Gly	Gly	Arg	Val	Ile	Lys	Gly
			100				105						110		
Pro	Asn	Asp	Pro	Gly	Lys	Leu	Ala	Glu	Phe	Val	Glu	Arg	Asn	Ser	Phe
		115				120					125				
Val	Phe	Phe	Cys	Asn	Pro	Asn	Asn	Pro	Asp	Gly	Lys	Phe	Tyr	Arg	Glu
	130					135					140				
Lys	Glu	Met	Lys	Pro	Leu	Leu	Asp	Ala	Ile	Gln	Asp	Thr	Asn	Ser	Ile

145					150					155				160
Leu	Ile	Leu	Asp	Glu	Ala	Phe	Ile	Asp	Phe	Val	Lys	Lys	Pro	Glu
				165					170					175
Pro	Glu	Gly	Glu	Asn	Ile	Ile	Arg	Leu	Arg	Thr	Phe	Thr	Lys	Ser
			180					185					190	
Gly	Leu	Pro	Gly	Val	Arg	Val	Gly	Tyr	Val	Ile	Gly	Phe	Val	Asp
		195					200					205		Ala
Phe	Arg	Ser	Val	Arg	Met	Pro	Trp	Ser	Ile	Gly	Ser	Thr	Gly	Val
	210					215					220			Ala
Phe	Leu	Glu	Phe	Leu	Leu	Lys	Asp	Asn	Phe	Lys	His	Leu	Arg	Lys
225				230						235				240
Leu	Pro	Leu	Ile	Trp	Lys	Glu	Lys	Glu	Arg	Ile	Glu	Lys	Glu	Leu
			245					250					255	
Val	Lys	Ser	Asp	Ala	Asn	Phe	Phe	Ile	Met	Lys	Val	Arg	Glu	Gly
			260					265					270	Ile
Ile	Glu	Lys	Leu	Lys	Glu	Asn	Gly	Ile	Leu	Val	Arg	Asp	Cys	Lys
		275				280						285		Ser
Phe	Gly	Leu	Pro	Gly	Tyr	Ile	Arg	Phe	Ser	Val	Arg	Arg	Arg	Glu
	290					295					300			Glu
Asn	Asp	Lys	Leu	Ile	Asn	Ile	Leu	Arg	Lys	Thr	Leu	Asn	Thr	
305					310					315				